#7

SEQUENCE LISTING

<110> Shimkets, Richard A.
        Fernandes, Elma R.
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        Gusev, Vladimir Y.
        Padigaru, Muralidhara
        Patturajan, Meera
        Shenoy, Suresh G.
        Spytek, Kimberly A.

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Cys Glu Ala Glu Glu Leu Arg Tyr Ser Leu His Val Gly Pro Trp Ser
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```
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```

<210> 4
<211> 267
<212> PRT
<213> human

<400> 4

```
Met Ser Asp Glu Asp Ser Cys Val Ala Cys Gly Ser Leu Arg Thr Ala
 1               5                  10                  15

Gly Pro Gln Ala Gly Ala Pro Ser Pro Trp Pro Trp Glu Ala Arg Leu
                20                  25                  30

Met His Gln Gly Gln Leu Ala Cys Gly Gly Ala Leu Val Ser Glu Glu
            35                  40                  45

Ala Val Leu Thr Ala Ala His Cys Phe Asn Gly Arg Gln Ala Pro Glu
        50                  55                  60

Glu Trp Ser Val Gly Leu Gly Thr Arg Pro Glu Glu Trp Gly Leu Lys
65                  70                  75                  80

Gln Leu Ile Leu His Gly Ala Tyr Thr His Pro Glu Gly Gly Tyr Asp
                85                  90                  95

Met Ala Leu Leu Leu Leu Ala Gln Pro Val Thr Leu Gly Ala Ser Leu
            100                 105                 110

Arg Ala Leu Cys Leu Pro Tyr Phe Asp His His Leu Pro Asp Gly Glu
            115                 120                 125

Arg Gly Trp Val Leu Gly Arg Ala Arg Pro Gly Ala Gly Ile Ser Ser
        130                 135                 140

Leu Gln Thr Val Pro Val Thr Leu Leu Gly Pro Arg Ala Cys Ser Arg
145                 150                 155                 160

Leu His Ala Ala Pro Gly Gly Asp Gly Ser Pro Ile Leu Pro Gly Met
                165                 170                 175

Val Cys Thr Ser Ala Val Gly Glu Leu Pro Ser Cys Glu Gly Leu Ser
            180                 185                 190

Gly Ala Pro Leu Val His Glu Val Arg Gly Thr Trp Phe Leu Ala Gly
            195                 200                 205

Leu His Ser Phe Gly Asp Ala Cys Gln Gly Pro Ala Arg Pro Ala Val
        210                 215                 220

Phe Thr Ala Leu Pro Ala Tyr Glu Asp Trp Val Ser Ser Leu Asp Trp
225                 230                 235                 240

Gln Val Tyr Phe Ala Glu Glu Pro Glu Pro Glu Ala Glu Pro Gly Ser
                245                 250                 255
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10

Cys Leu Ala Asn Ile Ser Gln Pro Thr Ser Cys
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<210> 5
<211> 1855
<212> DNA
<213> human

<400> 5
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<210> 6
<211> 405
<212> PRT
<213> human

<400> 6
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Thr Ala Val Leu Leu Ser Ala Gln Gly Gly Pro Val Gln Ser Lys Ser
             20                  25                  30


Pro Arg Phe Ala Ser Trp Asp Glu Met Asn Val Leu Ala His Gly Leu
```

11

```
           35                        40                        45
   Leu Gln Leu Gly Gln Gly Cys Ala Asn Thr Gly Ala His Pro Gln Ser
        50                    55                    60

   Ala Glu Arg Ala Gly Ala Arg Leu Ser Ala Cys Gly Ser Ala Cys Gln
   65                    70                    75                    80

   Gly Thr Glu Gly Ser Thr Asp Leu Pro Leu Ala Pro Glu Ser Arg Val
                     85                    90                    95

   Asp Pro Glu Val Leu His Ser Leu Gln Thr Gln Leu Lys Ala Gln Asn
                    100                   105                   110

   Ser Arg Ile Gln Gln Leu Phe His Lys Val Ala Gln Gln Gln Arg His
                    115                   120                   125

   Leu Glu Lys Gln His Leu Arg Ile Gln His Leu Gln Ser Gln Phe Gly
                    130                   135                   140

   Leu Leu Asp His Lys His Leu Asp His Glu Val Ala Lys Pro Ala Arg
   145                   150                   155                   160

   Arg Lys Arg Leu Pro Glu Met Ala Gln Pro Val Asp Pro Ala His Asn
                    165                   170                   175

   Val Ser Arg Leu His Arg Leu Pro Arg Asp Cys Gln Glu Leu Phe Gln
                    180                   185                   190

   Val Gly Glu Arg Gln Ser Gly Leu Phe Glu Ile Gln Pro Gln Gly Ser
                    195                   200                   205

   Pro Pro Phe Leu Val Asn Cys Lys Met Thr Ser Asp Gly Gly Trp Thr
   210                   215                   220

   Val Ile Gln Arg Arg His Asp Gly Ser Val Asp Phe Asn Arg Pro Trp
   225                   230                   235                   240

   Glu Ala Tyr Lys Ala Gly Phe Gly Asp Pro His Gly Glu Phe Trp Leu
                    245                   250                   255

   Gly Leu Glu Lys Val His Ser Met Met Gly Asp Arg Asn Ser Arg Leu
                    260                   265                   270

   Ala Val Gln Leu Arg Asp Trp Asp Gly Asn Ala Glu Leu Leu Gln Phe
                    275                   280                   285

   Ser Val His Leu Gly Gly Glu Asp Thr Ala Tyr Ser Leu Gln Leu Thr
        290                   295                   300

   Ala Pro Val Ala Gly Gln Leu Gly Ala Thr Thr Val Pro Pro Ser Gly
   305                   310                   315                   320

   Leu Ser Val Pro Phe Ser Thr Trp Asp Gln Asp His Asp Leu Arg Arg
                    325                   330                   335

   Asp Lys Asn Cys Ala Lys Ser Leu Ser Gly Gly Trp Trp Phe Gly Thr
```

12

```
                340                        345                        350

    Cys Ser His Ser Asn Leu Asn Gly Gln Tyr Phe Arg Ser Ile Pro Gln
            355                        360                    365

    Gln Arg Gln Lys Leu Lys Lys Gly Ile Phe Trp Lys Thr Trp Arg Gly
        370                        375                    380

    Arg Tyr Tyr Pro Leu Gln Ala Thr Thr Met Leu Ile Gln Pro Met Ala
    385                    390                    395                    400

    Ala Glu Ala Ala Ser
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<210> 7
<211> 3026
<212> DNA
<213> human

<400> 7

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13

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<210> 8
<211> 776
<212> PRT
<213> Homo sapiens

<400> 8

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Val Leu Leu Pro Ala Glu Ala Arg Glu Arg Ser Arg Gly Arg Ser Ile
            20                  25                  30

Ser Arg Gly Arg His Ala Arg Thr His Pro Gln Thr Ala Leu Leu Glu
        35                  40                  45

Ser Ser Cys Glu Asn Lys Arg Ala Asp Leu Val Phe Ile Ile Asp Ser
    50                  55                  60

Ser Arg Ser Val Asn Thr His Asp Tyr Ala Lys Val Lys Glu Phe Ile
65                  70                  75                  80

Val Asp Ile Leu Gln Phe Leu Asp Ile Gly Pro Asp Val Thr Arg Val
                85                  90                  95

Gly Leu Leu Gln Tyr Gly Ser Thr Val Lys Asn Glu Phe Ser Leu Lys
            100                 105                 110

Thr Phe Lys Arg Lys Ser Glu Val Glu Arg Ala Val Lys Arg Met Arg
        115                 120                 125

His Leu Ser Thr Gly Thr Met Thr Gly Leu Ala Ile Gln Tyr Ala Leu
    130                 135                 140

Asn Ile Ala Phe Ser Glu Ala Glu Gly Ala Arg Pro Leu Arg Glu Asn
145                 150                 155                 160

Val Pro Arg Val Ile Met Ile Val Thr Asp Gly Arg Pro Gln Asp Ser
                165                 170                 175

Val Ala Glu Val Ala Ala Lys Ala Arg Asp Thr Gly Ile Leu Ile Phe
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14

```
          180                    185                    190
  Ala Ile Gly Val Gly Gln Val Asp Phe Asn Thr Leu Lys Ser Ile Gly
          195                    200                    205

  Ser Glu Pro His Glu Asp His Val Phe Leu Val Ala Asn Phe Ser Gln
          210                    215                    220

  Ile Glu Thr Leu Thr Ser Val Phe Gln Lys Lys Leu Cys Thr Ala His
  225                    230                    235                    240

  Met Cys Ser Thr Leu Glu His Asn Cys Ala His Phe Cys Ile Asn Ile
                         245                    250                    255

  Pro Gly Ser Tyr Val Cys Arg Cys Lys Gln Gly Tyr Ile Leu Asn Ser
                         260                    265                    270

  Asp Gln Thr Thr Cys Arg Ile Gln Asp Leu Cys Ala Met Glu Asp His
                         275                    280                    285

  Asn Cys Glu Gln Leu Cys Val Asn Val Pro Gly Ser Phe Val Cys Glu
          290                    295                    300

  Cys Tyr Ser Gly Tyr Ala Leu Ala Glu Asp Gly Lys Arg Cys Val Ala
  305                    310                    315                    320

  Val Asp Tyr Cys Ala Ser Glu Asn His Gly Cys Glu His Glu Cys Val
                         325                    330                    335

  Asn Ala Asp Gly Ser Tyr Leu Cys Gln Cys His Glu Gly Phe Ala Leu
                         340                    345                    350

  Asn Pro Asp Glu Lys Thr Cys Thr Lys Ile Asp Tyr Cys Ala Ser Ser
                         355                    360                    365

  Asn His Gly Cys Gln Tyr Glu Cys Val Asn Thr Asp Asp Ser Tyr Ser
          370                    375                    380

  Cys His Cys Leu Lys Gly Phe Thr Leu Asn Pro Asp Lys Lys Thr Cys
  385                    390                    395                    400

  Arg Arg Ile Asn Tyr Cys Ala Leu Asn Lys Pro Gly Cys Glu His Glu
                         405                    410                    415

  Cys Val Asn Met Glu Glu Ser Tyr Tyr Cys Arg Cys His Arg Gly Tyr
                         420                    425                    430

  Thr Leu Asp Pro Asn Gly Lys Pro Cys Ser Arg Val Asp His Cys Ala
                         435                    440                    445

  Gln Gln Asp His Gly Cys Glu Gln Leu Cys Leu Asn Thr Glu Asp Ser
          450                    455                    460

  Phe Val Cys Gln Cys Ser Glu Gly Phe Leu Ile Asn Glu Asp Leu Lys
  465                    470                    475                    480

  Thr Cys Ser Arg Val Asp Tyr Cys Leu Leu Ser Asp His Gly Cys Glu
```

15

```
              485                      490                      495
Tyr Ser Cys Val Asn Met Asp Arg Ser Phe Ala Cys Gln Cys Pro Glu
        500                      505                510

Gly His Val Leu Arg Ser Asp Gly Lys Thr Cys Ala Lys Leu Asp Ser
        515                      520                525

Cys Ala Leu Gly Asp His Gly Cys Glu His Ser Cys Val Ser Ser Glu
        530                      535                540

Asp Ser Phe Val Cys Gln Cys Phe Glu Gly Tyr Ile Leu Arg Glu Asp
545                      550                      555                560

Gly Lys Thr Cys Arg Arg Lys Asp Val Cys Gln Ala Ile Asp His Gly
                565                      570                575

Cys Glu His Ile Cys Val Asn Ser Asp Asp Ser Tyr Thr Cys Glu Cys
            580                      585                590

Leu Glu Gly Phe Arg Leu Thr Glu Asp Gly Lys Arg Cys Arg Ile Ser
        595                      600                605

Ser Gly Lys Asp Val Cys Lys Ser Thr His His Gly Cys Glu His Ile
    610                      615                620

Cys Val Asn Asn Gly Asn Ser Tyr Ile Cys Lys Cys Ser Glu Gly Phe
625                      630                      635                640

Val Leu Ala Glu Asp Gly Arg Arg Cys Lys Lys Cys Thr Glu Gly Pro
                645                      650                655

Ile Asp Leu Val Phe Val Ile Asp Gly Ser Lys Ser Leu Gly Glu Glu
            660                      665                670

Asn Phe Glu Val Val Lys Gln Phe Val Thr Gly Ile Ile Asp Ser Leu
        675                      680                685

Thr Ile Ser Pro Lys Ala Ala Arg Val Gly Leu Leu Gln Tyr Ser Thr
    690                      695                700

Gln Val His Thr Glu Phe Thr Leu Arg Asn Phe Asn Ser Ala Lys Asp
705                      710                      715                720

Met Lys Lys Ala Val Ala His Met Lys Tyr Met Gly Lys Gly Ser Met
                725                      730                735

Thr Gly Leu Ala Leu Lys His Met Phe Glu Arg Ser Phe Thr Gln Gly
            740                      745                750

Glu Gly Ala Arg Pro Leu Phe His Lys Gly Ala Gln Ser Ser His Cys
        755                      760                765

Val His Arg Arg Thr Gly Ser Gly
    770                      775
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16

<210> 9
<211> 3447
<212> DNA
<213> human

<400> 9

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aaccttataa tgttccagaa ccttgcaaac gaagaagtaa gaaattaac acagcgctta 2880
gaagaaatga cacagagaat ggaagccctg gaaaatcgcc tgagatacag atgaagatta 2940
gaaatcgcga cacatttgta gtcattgtat cacggattac aatgaacgca gtgcagagcc 3000
ccaaagctca ggctattgtt aaatcaataa tgttgtgaag taaaacaatc agtactgaga 3060
```

```
aacctggttt gccacagaac aaagacaaga agtatacact aacttgtata aatttatcta 3120
ggaaaaaaat ccttcagaat tctaagatga atttaccagg tgagaatgaa taagctatgc 3180
aaggtatttt gtaatatact gtggacacaa cttgcttctg ccctcatcctg ccttagtgtg 3240
caatctcatt tgactatacg ataaagtttg cacagtctta cttctgtaga acactggcca 3300
taggaaatgc tgttttttttg tactggactt taccttgata tatgtatatg gatgtatgca 3360
taaaatcata ggacatatgt acttgtggaa caagttggat tttttataca atattaaaat 3420
tcaccacttc agagaaaagt aaaaaaa                                      3447
```

<210> 10
<211> 959
<212> PRT
<213> human

<400> 10

```
Met Glu Lys Met Leu Ala Gly Cys Phe Leu Leu Ile Leu Gly Gln Ile
1               5                   10                  15

Val Leu Leu Pro Cys Glu Ala Arg Glu Arg Ser Arg Gly Arg Ser Ile
            20                  25                  30

Ser Arg Gly Arg His Ala Arg Thr His Pro Gln Thr Ala Leu Leu Glu
        35                  40                  45

Ser Ser Cys Glu Asn Lys Arg Ala Asp Leu Val Phe Ile Ile Asp Ser
    50                  55                  60

Ser Arg Ser Val Asn Thr His Asp Tyr Ala Lys Val Lys Glu Phe Ile
65                  70                  75                  80

Val Asp Ile Leu Gln Phe Leu Asp Ile Gly Pro Asp Val Thr Arg Val
                85                  90                  95

Gly Leu Leu Gln Tyr Gly Ser Thr Val Lys Asn Glu Phe Ser Leu Lys
            100                 105                 110

Thr Phe Lys Arg Lys Ser Glu Val Glu Arg Ala Val Lys Arg Met Arg
        115                 120                 125

His Leu Ser Thr Gly Thr Met Thr Gly Leu Ala Ile Gln Tyr Ala Leu
    130                 135                 140

Asn Ile Ala Phe Ser Glu Ala Glu Gly Ala Arg Pro Leu Arg Glu Asn
145                 150                 155                 160

Val Pro Arg Val Ile Met Ile Val Thr Asp Gly Arg Pro Gln Asp Ser
                165                 170                 175

Val Ala Glu Val Ala Ala Lys Ala Arg Asp Thr Gly Ile Leu Ile Phe
            180                 185                 190

Ala Ile Gly Val Gly Gln Val Asp Phe Asn Thr Leu Lys Ser Ile Gly
        195                 200                 205

Ser Glu Pro His Glu Asp His Val Phe Leu Val Ala Asn Phe Ser Gln
    210                 215                 220
```

18

```
Ile Glu Thr Leu Thr Ser Val Phe Gln Lys Lys Leu Cys Thr Ala His
225                 230                 235                 240

Met Cys Ser Thr Leu Glu His Asn Cys Ala His Phe Cys Ile Asn Ile
                245                 250                 255

Pro Gly Ser Tyr Val Cys Arg Cys Lys Gln Gly Tyr Ile Leu Asn Ser
                260                 265                 270

Asp Gln Thr Thr Cys Arg Ile Gln Asp Leu Cys Ala Met Glu Asp His
        275                 280                 285

Asn Cys Glu Gln Leu Cys Val Asn Val Pro Gly Ser Phe Val Cys Glu
        290                 295                 300

Cys Tyr Ser Gly Tyr Ala Leu Ala Glu Asp Gly Lys Arg Cys Val Ala
305                 310                 315                 320

Val Asp Tyr Cys Ala Ser Glu Asn His Gly Cys Glu His Glu Cys Val
                325                 330                 335

Asn Ala Asp Gly Ser Tyr Leu Cys Gln Cys His Glu Gly Phe Ala Leu
                340                 345                 350

Asn Pro Asp Glu Lys Thr Cys Thr Lys Ile Asp Tyr Cys Ala Ser Ser
                355                 360                 365

Asn His Gly Cys Gln Tyr Glu Cys Val Asn Thr Asp Asp Ser Tyr Ser
        370                 375                 380

Cys His Cys Leu Lys Gly Phe Thr Leu Asn Pro Asp Lys Lys Thr Cys
385                 390                 395                 400

Arg Arg Ile Asn Tyr Cys Ala Leu Asn Lys Pro Gly Cys Glu His Glu
                405                 410                 415

Cys Val Asn Met Glu Glu Ser Tyr Tyr Cys Arg Cys His Arg Gly Tyr
                420                 425                 430

Thr Leu Asp Pro Asn Gly Lys Pro Cys Ser Arg Val Asp His Cys Ala
        435                 440                 445

Gln Gln Asp His Gly Cys Glu Gln Leu Cys Leu Asn Thr Glu Asp Ser
        450                 455                 460

Phe Val Cys Gln Cys Ser Glu Gly Phe Leu Ile Asn Glu Asp Leu Lys
465                 470                 475                 480

Thr Cys Ser Arg Val Asp Tyr Cys Leu Leu Ser Asp His Gly Cys Glu
                485                 490                 495

Tyr Ser Cys Val Asn Met Asp Arg Ser Phe Ala Cys Gln Cys Pro Glu
                500                 505                 510

Gly His Val Leu Arg Ser Asp Gly Lys Thr Cys Ala Lys Leu Asp Ser
                515                 520                 525
```

19

```
Cys Ala Leu Gly Asp His Gly Cys Glu His Ser Cys Val Ser Ser Glu
    530             535             540

Asp Ser Phe Val Cys Gln Cys Phe Glu Gly Tyr Ile Leu Arg Glu Asp
545             550             555             560

Gly Lys Thr Cys Arg Arg Lys Asp Val Cys Gln Ala Ile Asp His Gly
            565             570             575

Cys Glu His Ile Cys Val Asn Ser Asp Asp Ser Tyr Thr Cys Glu Cys
        580             585             590

Leu Glu Gly Phe Arg Leu Thr Glu Asp Gly Lys Arg Cys Arg Ile Ser
        595             600             605

Ser Gly Lys Asp Val Cys Lys Ser Thr His His Gly Cys Glu His Ile
    610             615             620

Cys Val Asn Asn Gly Asn Ser Tyr Ile Cys Lys Cys Ser Glu Gly Phe
625             630             635             640

Val Leu Ala Glu Asp Gly Arg Arg Cys Lys Lys Cys Thr Glu Gly Pro
            645             650             655

Ile Asp Leu Val Phe Val Ile Asp Gly Ser Lys Ser Leu Gly Glu Glu
        660             665             670

Asn Phe Glu Val Val Lys Gln Phe Val Thr Gly Ile Ile Asp Ser Leu
        675             680             685

Thr Ile Ser Pro Lys Ala Ala Arg Val Gly Leu Leu Gln Tyr Ser Thr
    690             695             700

Gln Val His Thr Glu Phe Thr Leu Arg Asn Phe Asn Ser Ala Lys Asp
705             710             715             720

Met Lys Lys Ala Val Ala His Met Lys Tyr Met Gly Lys Gly Ser Met
            725             730             735

Thr Gly Leu Ala Leu Lys His Met Phe Glu Arg Ser Phe Thr Gln Gly
        740             745             750

Glu Gly Ala Arg Pro Phe Ser Thr Arg Val Pro Arg Ala Ala Ile Val
    755             760             765

Phe Thr Asp Gly Arg Ala Gln Asp Asp Val Ser Glu Trp Ala Ser Lys
    770             775             780

Ala Lys Ala Asn Gly Ile Thr Met Tyr Ala Val Gly Val Gly Lys Ala
785             790             795             800

Ile Glu Glu Glu Leu Gln Glu Ile Ala Ser Glu Pro Thr Asn Lys His
            805             810             815

Leu Phe Tyr Ala Glu Asp Phe Ser Thr Met Asp Glu Ile Ser Glu Lys
        820             825             830
```

```
Leu Lys Lys Gly Ile Cys Glu Ala Leu Glu Asp Ser Asp Gly Arg Gln
    835             840             845

Asp Ser Pro Ala Gly Glu Leu Pro Lys Thr Val Gln Gln Pro Thr Glu
    850             855             860

Ser Glu Pro Val Thr Ile Asn Ile Gln Asp Leu Leu Ser Cys Ser Asn
865             870             875             880

Phe Ala Val Gln His Arg Tyr Leu Phe Glu Glu Asp Asn Leu Leu Arg
            885             890             895

Ser Thr Gln Lys Leu Ser His Ser Thr Lys Pro Ser Gly Ser Pro Leu
            900             905             910

Glu Glu Lys His Asp Gln Cys Lys Cys Glu Asn Leu Ile Met Phe Gln
            915             920             925

Asn Leu Ala Asn Glu Glu Val Arg Lys Leu Thr Gln Arg Leu Glu Glu
    930             935             940

Met Thr Gln Arg Met Glu Ala Leu Glu Asn Arg Leu Arg Tyr Arg
945             950             955
```

```
<210> 11
<211> 967
<212> DNA
<213> human

<400> 11
cggcccttct cacactcctg ccctgctgat gtggaacggg gtttggggtt ctgcagggct 60
attgtctgcg ctggggaagg ggacaggccg ggaccgggac ctccgctcgc agccggccgc 120
accagcagga cagctggcct gaagctcaga gccggggcgt gcgccatggc cccacactgg 180
gctgtctggc tgctggcagc aaggctgtgg ggcctgggca ttggggctga ggtgtggtgg 240
aaccttgtgc cgcgtaagac agtgtcttct ggggagctgg ccacggtagt acggcggttc 300
tcccagaccg gcatccagga cttcctgaca ctgacgctga cggagcccac tgggcttctg 360
tacgtgggcg cccgagaggc cctgtttgcc ttcagcatgg aggccctgga gctgcaagga 420
gcgatctcct gggaggcccc cgtggagaag aagactgagt gtatccagaa agggaagaac 480
aaccagaccg agtgcttcaa cttcatccgc ttcctgcagc cctacaatgc ctcccacctg 540
tacgtctgtg gcacctacgc cttccagccc aagtgcacct acgtcaacat gctcaccttc 600
actttggagc atggagagtt tgaagatggg aagggcaagt gtccctatga cccagctaag 660
ggccatgctg gccttcttgt ggatggtgag ctgtactcgg ccacactcaa caacttcctg 720
ggcacggaac ccattatcct gcgtaacatg gggccccacc actccatgaa gacagagtac 780
ctggcctttt ggctcaacga acctcacttt gtaggctctg cctatgtacc tgagagggtg 840
ggcctgctgt ggacaatggc atactctctt ccagccctag gaggagggct cctaacagtg 900
taacttattg tgtccccgcg tatttatttg ttgtaaatat ttgagtattt ttatattgac 960
aaataaa                                                          967
```

```
<210> 12
<211> 245
<212> PRT
<213> human

<400> 12
Met Ala Pro His Trp Ala Val Trp Leu Leu Ala Ala Arg Leu Trp Gly
```

21

```
       1                   5                   10                  15
     Leu Gly Ile Gly Ala Glu Val Trp Trp Asn Leu Val Pro Arg Lys Thr
                 20                  25                  30

     Val Ser Ser Gly Glu Leu Ala Thr Val Val Arg Arg Phe Ser Gln Thr
                 35                  40                  45

     Gly Ile Gln Asp Phe Leu Thr Leu Thr Leu Thr Glu Pro Thr Gly Leu
             50                  55                  60

     Leu Tyr Val Gly Ala Arg Glu Ala Leu Phe Ala Phe Ser Met Glu Ala
     65                  70                  75                  80

     Leu Glu Leu Gln Gly Ala Ile Ser Trp Glu Ala Pro Val Glu Lys Lys
                     85                  90                  95

     Thr Glu Cys Ile Gln Lys Gly Lys Asn Asn Gln Thr Glu Cys Phe Asn
                 100                 105                 110

     Phe Ile Arg Phe Leu Gln Pro Tyr Asn Ala Ser His Leu Tyr Val Cys
             115                 120                 125

     Gly Thr Tyr Ala Phe Gln Pro Lys Cys Thr Tyr Val Asn Met Leu Thr
         130                 135                 140

     Phe Thr Leu Glu His Gly Glu Phe Glu Asp Gly Lys Gly Lys Cys Pro
     145                 150                 155                 160

     Tyr Asp Pro Ala Lys Gly His Ala Gly Leu Leu Val Asp Gly Glu Leu
                 165                 170                 175

     Tyr Ser Ala Thr Leu Asn Asn Phe Leu Gly Thr Glu Pro Ile Ile Leu
                 180                 185                 190

     Arg Asn Met Gly Pro His His Ser Met Lys Thr Glu Tyr Leu Ala Phe
             195                 200                 205

     Trp Leu Asn Glu Pro His Phe Val Gly Ser Ala Tyr Val Pro Glu Arg
         210                 215                 220

     Val Gly Leu Leu Trp Thr Met Ala Tyr Ser Leu Pro Ala Leu Gly Gly
     225                 230                 235                 240

     Gly Leu Leu Thr Val
                 245
```

<210> 13
<211> 1359
<212> DNA
<213> human

<400> 13
ggcaccaggc cttccggaga gacgcagtcg gctgccaccc cgggatgggt cgctggtgcc 60
agaccgtcgc gcgcgggcag cgcccccgga cgtctgcccc ctcccgcgcc ggtgccctgc 120
tgctgctgct tctgttgctg aggtctgcag gttgctgggg cgcagggga agccccgggg 180

22

```
cgctgtccac tgctgatccc gccgaccaga gcgtccagtg tgtccccaag gccacctgtc 240
cttccagccg gcctcgcctt ctctggcaga ccccgaccac ccagacactg ccctcgacca 300
ccatggagac ccaattccca gtttctgaag gcaaagtcga cccataccgc tcctgtggct 360
tttcctacga gcaggacccc accctcaggg acccagaagc cgtggctcgg cggtggccct 420
ggatggtcag cgtgcgggcc aatggcacac acatctgtgc cggcaccatc attgcctccc 480
agtgggtgct gactgtggcc cactgcctga tctggcgtga tgttatctac tcagtgaggg 540
tggggagtcc gtggattgac cagatgacgc agaccgcctc cgatgtcccg gtgctccagg 600
tcatcatgca tagcaggtac cgggcccagc ggttctggtc ctgggtgggc caggccaacg 660
acatcggcct cctcaagctc aagcaggaac tcaagtacag caattacgtg cggcccatct 720
gcctgcctgg cacggactat gtgttgaagg accattcccg ctgcactgtg acgggctggg 780
gactttccaa ggctgacggc atgtggcctc agttccggac cattcaggag aaggaagtca 840
tcatcctgaa caacaaagag tgtgacaatt ctaccacaa cttcaccaaa atccccactc 900
tggttcagat catcaagtcc cagatgatgt gtgcggagga cacccacagg gagaagttct 960
gctatgagct aactggagag ccccttggtct gctccatgga gggcacgtgg tacctggtgg 1020
gattggtgag ctgggggtgca ggctgccaga agagcgaggc cccacccatc tacctacagg 1080
tctcctccta ccaacactgg atctgggact gcctcaacgg gcaggccctg gccctgccag 1140
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gactctgtgt gccctccctc acttgtgggc cccccttgcc tccgtgccca ggttgctgtg 1260
ggtgcagctg tcacagccct gagagtcagg gtggagatga ggtgctcaat taaacattac 1320
tgttttccat gtaaaaaaaa aaaaaaaaa aaaaaaaaa 1359
```

<210> 14
<211> 385
<212> PRT
<213> human

<400> 14

```
Met Gly Arg Trp Cys Gln Thr Val Ala Arg Gly Gln Arg Pro Arg Thr
1               5                   10                  15

Ser Ala Pro Ser Arg Ala Gly Ala Leu Leu Leu Leu Leu Leu Leu Leu
            20                  25                  30

Arg Ser Ala Gly Cys Trp Gly Ala Gly Glu Ala Pro Gly Ala Leu Ser
        35                  40                  45

Thr Ala Asp Pro Ala Asp Gln Ser Val Gln Cys Val Pro Lys Ala Thr
    50                  55                  60

Cys Pro Ser Ser Arg Pro Arg Leu Leu Trp Gln Thr Pro Thr Thr Gln
65                  70                  75                  80

Thr Leu Pro Ser Thr Thr Met Glu Thr Gln Phe Pro Val Ser Glu Gly
                85                  90                  95

Lys Val Asp Pro Tyr Arg Ser Cys Gly Phe Ser Tyr Glu Gln Asp Pro
            100                 105                 110

Thr Leu Arg Asp Pro Glu Ala Val Ala Arg Arg Trp Pro Trp Met Val
        115                 120                 125

Ser Val Arg Ala Asn Gly Thr His Ile Cys Ala Gly Thr Ile Ile Ala
    130                 135                 140

Ser Gln Trp Val Leu Thr Val Ala His Cys Leu Ile Trp Arg Asp Val
145                 150                 155                 160
```

23

```
Ile Tyr Ser Val Arg Val Gly Ser Pro Trp Ile Asp Gln Met Thr Gln
            165                 170                 175

Thr Ala Ser Asp Val Pro Val Leu Gln Val Ile Met His Ser Arg Tyr
            180                 185                 190

Arg Ala Gln Arg Phe Trp Ser Trp Val Gly Gln Ala Asn Asp Ile Gly
            195                 200                 205

Leu Leu Lys Leu Lys Gln Glu Leu Lys Tyr Ser Asn Tyr Val Arg Pro
    210                 215                 220

Ile Cys Leu Pro Gly Thr Asp Tyr Val Leu Lys Asp His Ser Arg Cys
225                 230                 235                 240

Thr Val Thr Gly Trp Gly Leu Ser Lys Ala Asp Gly Met Trp Pro Gln
            245                 250                 255

Phe Arg Thr Ile Gln Glu Lys Glu Val Ile Ile Leu Asn Asn Lys Glu
            260                 265                 270

Cys Asp Asn Phe Tyr His Asn Phe Thr Lys Ile Pro Thr Leu Val Gln
            275                 280                 285

Ile Ile Lys Ser Gln Met Met Cys Ala Glu Asp Thr His Arg Glu Lys
    290                 295                 300

Phe Cys Tyr Glu Leu Thr Gly Glu Pro Leu Val Cys Ser Met Glu Gly
305                 310                 315                 320

Thr Trp Tyr Leu Val Gly Leu Val Ser Trp Gly Ala Gly Cys Gln Lys
            325                 330                 335

Ser Glu Ala Pro Pro Ile Tyr Leu Gln Val Ser Ser Tyr Gln His Trp
            340                 345                 350

Ile Trp Asp Cys Leu Asn Gly Gln Ala Leu Ala Leu Pro Ala Pro Ser
            355                 360                 365

Arg Thr Leu Leu Leu Ala Leu Pro Leu Pro Leu Ser Leu Leu Ala Ala
    370                 375                 380

Leu
385


<210> 15
<211> 1445
<212> DNA
<213> human

<400> 15
cacccctctg cctgccccag cccgcccatc gcttcccctt tggagcctcc tgctgggcca 60
ctggctggga tcaggacacc agtgatggta agtgctggcc agactgaag  tcgggagagg 120
cactctgctt gcccagcgtc acagtcttag ctcccaactg tcctggcttc cagtctccct 180
tgcttcccag atcccagact ctagccccag ccccgtctct ttcaccagct cctgggaccc 240
```

24

```
tacgcaatct gcgcctgcgt ctcatcagtc gccccacatg taactgtatc tacaaccagc 300
tgcaccagcg acacctgtcc aacccggccc ggcctgggat gctatgtggg ggcccccagc 360
ctggggtgca gggcccctgt caggtctgat aggggagaaga gaaggagcag aaggggaggg 420
gcctaaccct gggctggggg ttggactcac aggactgggg gaaagagctg caatcagagg 480
gtgtctgcca tagctgggct caggcatctg tccttggctt tgttgcctgg ctccaggag 540
attccggggg ccctgtgctg tgcctcgagc ctgacggaca ctgggttcag gctggcatca 600
tcagctttgc atcaagctgt gcccaggagg acgctcctgt gctgctgacc aacacagctg 660
ctcacagttc ctggctgcag gctcgagttc aggggggcagc tttcctggcc cagagcagcag 720
agaccccgga gatgagtgat gaggacagct gtgtagcctg tggatccttg aggacagcag 780
gtccccaggc aggagcaccc tccccatggc cctgggaggc caggctgatg caccagggac 840
agctggcctg tggcggagcc ctggtgtcag aggaggcggt gctaactgct gcccactgct 900
tcattgggcg ccaggcccca gaggaatgga gcgtagggct ggggaccaga ccggaggagt 960
ggggcctgaa gcagctcatc ctgcatggag cctacaccca ccctgagggg ggctacgaca 1020
tggccctcct gctgctggcc cagcctgtga cactgggagc cagcctgcgg ccctctgcc 1080
tgccctatgc tgaccaccac ctgcctgatg gggagcgtgg ctgggttctg ggacgggccc 1140
gcccaggagc aggcatcagc tccctccaga cagtgcccgt gaccctcctg gggcctaggg 1200
cctgcagccg gctgcatgca gctcctgggg gtgatggcag ccctattctg ccggggatgg 1260
tgtgtaccag tgctgtgggt gagctgccca gctgtgaggt gagccccagg cccccacacc 1320
ttacctaaca ggccctggc atcccctcac ccaatagctc aagaacggac cttccaggct 1380
tggcctctgg acccacctcc cacctgaagc taagcctttt tgccaattag ccccaaaca 1440
gccag                                                             1445
```

<210> 16
<211> 198
<212> PRT
<213> human

<400> 16

```
Met Ser Asp Glu Asp Ser Cys Val Ala Cys Gly Ser Leu Arg Thr Ala
  1               5                   10                  15

Gly Pro Gln Ala Gly Ala Pro Ser Pro Trp Pro Trp Glu Ala Arg Leu
              20                  25                  30

Met His Gln Gly Gln Leu Ala Cys Gly Gly Ala Leu Val Ser Glu Glu
          35                  40                  45

Ala Val Leu Thr Ala Ala His Cys Phe Ile Gly Arg Gln Ala Pro Glu
      50                  55                  60

Glu Trp Ser Val Gly Leu Gly Thr Arg Pro Glu Glu Trp Gly Leu Lys
 65                  70                  75                  80

Gln Leu Ile Leu His Gly Ala Tyr Thr His Pro Glu Gly Gly Tyr Asp
                  85                  90                  95

Met Ala Leu Leu Leu Leu Ala Gln Pro Val Thr Leu Gly Ala Ser Leu
             100                 105                 110

Arg Pro Leu Cys Leu Pro Tyr Ala Asp His His Leu Pro Asp Gly Glu
         115                 120                 125

Arg Gly Trp Val Leu Gly Arg Ala Arg Pro Gly Ala Gly Ile Ser Ser
     130                 135                 140

Leu Gln Thr Val Pro Val Thr Leu Leu Gly Pro Arg Ala Cys Ser Arg
```

25

```
145                 150                 155                 160

Leu His Ala Ala Pro Gly Gly Asp Gly Ser Pro Ile Leu Pro Gly Met
                165                 170                 175

Val Cys Thr Ser Ala Val Gly Glu Leu Pro Ser Cys Glu Val Ser Pro
                180                 185                 190

Arg Pro Pro His Leu Thr
                195
```

<210> 17
<211> 1600
<212> DNA
<213> human

<400> 17

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cttaacagcc acttgtttca tcccacctgg gcattaggtt gacttcaaag atgcctcagt 60
tactgcaaaa cattaatggg atcatcgagg ccttcaggcg ctatgcaagg acggagggca 120
actgcacagc gctcacccga ggggagctga aaagactctt ggagcaagag tttgccgatg 180
tgattgtgaa accccacgat ccagcaactg tggatgaggt cctgcgtctg ctggatgaag 240
accacacagg gactgtggaa ttcaaggaat tcctggtctt agtgtttaaa gttgcccagg 300
cctgtttcaa gacactgagc gagagtgctg agggagcctg cggctctcaa gagtctggaa 360
gcctccactc tggggcctcg caggagctgg gcgaaggaca gagaagtggc actgaagtgg 420
gaagggcggg gaaagggcag cattatgagg ggagcagcca cagacagagc cagcagggtt 480
ccagagggca gaacaggcct ggggttcaga cccagggtca ggccactggc tctgcgtggg 540
tcagcagcta tgacaggcaa gctgagtccc agagccagga aagaataagc ccgcagatac 600
aactctctgg gcagacagag cagacccaga aagctggaga aggcaagagg aatcagacaa 660
cagagatgag gccagagaga cagccacaga ccagggaaca ggacagagcc caccagacag 720
gtgagactgt gactggatct ggaactcaga cccaggcagg tgccacccag actgtggagc 780
aggacagcag ccaccagaca ggaagcacca gcacccagac acaggagtcc accaatggcc 840
agaacagagg gactgagatc cacggtcaag gcaggagcca gaccagccag gctgtgacag 900
gaggacacac tcagatacag gcaggtcac acaccgagac tgtggagcag acagaagcc 960
aaactgtaag ccacggaggg gctagagaac agggacagac ccagacgcag ccaggcagtg 1020
gtcaaagatg gatgcaagtg agcaaccctg aggcaggaga gacagtaccg ggaggacagg 1080
cccagactgg ggcaagcact gagtcaggaa ggcaggagtg gagcagcact cacccaaggc 1140
gctgtgtgac agaagggcag ggagacagac agcccacagt ggttggtgag gaatggggttg 1200
atgaccactc aagggagaca gtgatcctca ggctggacca gggcaacttg cataccagtg 1260
tttcctcagc acagggccag gatgcagccc agtcagaaga gaagcgaggc atcacagcta 1320
gagagctgta ttcctacttg agaagcacca agccatgact ccccgactc caatgtccag 1380
tactggaaga agacagctgg agagagtttg gcttgtcctg catggccaat ccagtgggtg 1440
catccctgga catcagctct tcattatgca gcttcccttt taggtctttc tcaatgagat 1500
aatttctgca aggagctttc tatcctgaac tcttctttct tacctgcttt gcggtgcaga 1560
ccctctcagg agcaggaaga ctcagaacaa gtcaccccctt            1600
```

<210> 18
<211> 435
<212> PRT
<213> human

<400> 18

```
Met Pro Gln Leu Leu Gln Asn Ile Asn Gly Ile Ile Glu Ala Phe Arg
  1               5                  10                  15

Arg Tyr Ala Arg Thr Glu Gly Asn Cys Thr Ala Leu Thr Arg Gly Glu
```

26

```
                    20                      25                      30
Leu Lys Arg Leu Leu Glu Gln Glu Phe Ala Asp Val Ile Val Lys Pro
         35                  40                  45

His Asp Pro Ala Thr Val Asp Glu Val Leu Arg Leu Leu Asp Glu Asp
         50                  55                  60

His Thr Gly Thr Val Glu Phe Lys Glu Phe Leu Val Leu Val Phe Lys
65                  70                  75                  80

Val Ala Gln Ala Cys Phe Lys Thr Leu Ser Glu Ser Ala Glu Gly Ala
             85                  90                  95

Cys Gly Ser Gln Glu Ser Gly Ser Leu His Ser Gly Ala Ser Gln Glu
            100                 105                 110

Leu Gly Glu Gly Gln Arg Ser Gly Thr Glu Val Gly Arg Ala Gly Lys
        115                 120                 125

Gly Gln His Tyr Glu Gly Ser Ser His Arg Gln Ser Gln Gln Gly Ser
    130                 135                 140

Arg Gly Gln Asn Arg Pro Gly Val Gln Thr Gln Gly Gln Ala Thr Gly
145                 150                 155                 160

Ser Ala Trp Val Ser Ser Tyr Asp Arg Gln Ala Glu Ser Gln Ser Gln
                165                 170                 175

Glu Arg Ile Ser Pro Gln Ile Gln Leu Ser Gly Gln Thr Glu Gln Thr
            180                 185                 190

Gln Lys Ala Gly Glu Gly Lys Arg Asn Gln Thr Thr Glu Met Arg Pro
        195                 200                 205

Glu Arg Gln Pro Gln Thr Arg Glu Gln Asp Arg Ala His Gln Thr Gly
    210                 215                 220

Glu Thr Val Thr Gly Ser Gly Thr Gln Thr Gln Ala Gly Ala Thr Gln
225                 230                 235                 240

Thr Val Glu Gln Asp Ser Ser His Gln Thr Gly Ser Thr Ser Thr Gln
                245                 250                 255

Thr Gln Glu Ser Thr Asn Gly Gln Asn Arg Gly Thr Glu Ile His Gly
            260                 265                 270

Gln Gly Arg Ser Gln Thr Ser Gln Ala Val Thr Gly Gly His Thr Gln
        275                 280                 285

Ile Gln Ala Gly Ser His Thr Glu Thr Val Glu Gln Asp Arg Ser Gln
    290                 295                 300

Thr Val Ser His Gly Gly Ala Arg Glu Gln Gly Gln Thr Gln Thr Gln
305                 310                 315                 320

Pro Gly Ser Gly Gln Arg Trp Met Gln Val Ser Asn Pro Glu Ala Gly
```

27

```
                     325                      330                       335

Glu Thr Val Pro Gly Gly Gln Ala Gln Thr Gly Ala Ser Thr Glu Ser
            340                 345                 350

Gly Arg Gln Glu Trp Ser Ser Thr His Pro Arg Arg Cys Val Thr Glu
            355                 360                 365

Gly Gln Gly Asp Arg Gln Pro Thr Val Val Gly Glu Glu Trp Val Asp
        370                 375                 380

Asp His Ser Arg Glu Thr Val Ile Leu Arg Leu Asp Gln Gly Asn Leu
385                         390                 395                 400

His Thr Ser Val Ser Ser Ala Gln Gly Gln Asp Ala Ala Gln Ser Glu
            405                 410                 415

Glu Lys Arg Gly Ile Thr Ala Arg Glu Leu Tyr Ser Tyr Leu Arg Ser
            420                 425                 430

Thr Lys Pro
        435
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<210> 19
<211> 42
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<210> 20
<211> 37
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
     Oligonucleotide Primer

<400> 20
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<210> 21
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
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Oligonucleotide Primer

<400> 21
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<210> 22
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
      Oligonucleotide Primer

<400> 22
ctcgtcgggc ccctgatcag cgggtttaaa c   31

<210> 23
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
      Oligonucleotide Primer

<400> 23
ctcgtcggat cctggggcgc aggggaagcc ccggg   35

<210> 24
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
      Oligonucleotide Primer

<400> 24
ctcgtcctcg aggagggcag caaggaggct gaggggcag   39

<210> 25
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
      Oligonucleotide Primer

<400> 25
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<210> 26
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<220>
<223> Description of Artificial Sequence:
      Oligonucleotide Primer

<400> 26
agaggctctt ggcgcagtt                                              19


<210> 27
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
      Oligonucleotide Primer

<400> 27
accaggatca cgacctccgc agg                                         23


<210> 28
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
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<400> 28
gcctggcacg gactatgtgt                                             20


<210> 29
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
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<400> 29
gccgtcagcc ttggaaagt                                              19


<210> 30
<211> 22
<212> DNA
<213> Artificial Sequence
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<210> 30
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
      Oligonucleotide Primer

<400> 30
ccattcccgc tgcactgtga cg   22

<210> 31
<211> 22
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<220>
<223> Description of Artificial Sequence:
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<400> 31
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<210> 32
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
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<400> 32
tggtcctaac tgcaccacag tct   23

<210> 33
<211> 28
<212> DNA
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<220>
<223> Description of Artificial Sequence:
      Oligonucleotide Primer

<400> 33
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<210> 34
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
      Oligonucleotide Primer

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<400> 34
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<210> 35
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
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<400> 35
ttctgactgg gctgcatcc                                               19


<210> 36
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
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<400> 36
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<210> 37
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
      Oligonucleotide Primer

<400> 37
tgtgctcagc acatggtcta                                              20


<210> 38
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
      Oligonucleotide Primer

<400> 38
acacctgctc agggaaaacg acagaa                                       26


<210> 39
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<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
      Oligonucleotide Primer

<400> 39
tcgtgctcgt atctgtttcc                                                       20


<210> 40
<211> 4810
<212> DNA
<213> human

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<210> 41
<211> 1588
<212> PRT
<213> human

<400> 41

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 1               5                  10                  15

Cys Ala His Val Glu Gly Trp Thr Thr Leu His Thr Asn Cys Lys Gln
            20                  25                  30

Ala Glu Arg Pro Asn Asn Gln Gln Asn Cys Phe Lys Val Cys Asp Trp
```

34

```
                35                      40                       45

His Lys Glu Leu Tyr Asp Trp Arg Leu Gly Pro Trp Asn Gln Cys Gln
    50                      55                      60

Pro Val Ile Ser Lys Ser Leu Glu Lys Pro Leu Glu Cys Ile Lys Gly
65                      70                      75                      80

Glu Glu Gly Ile Gln Val Arg Glu Ile Ala Cys Ile Gln Lys Asp Lys
                    85                      90                      95

Asp Ile Pro Ala Glu Asp Ile Ile Cys Glu Tyr Phe Glu Pro Lys Pro
                100                     105                     110

Leu Leu Glu Gln Ala Cys Leu Ile Pro Cys Gln Gln Asp Cys Ile Val
        115                     120                     125

Ser Glu Phe Ser Ala Trp Ser Glu Cys Ser Lys Thr Cys Gly Ser Gly
        130                     135                     140

Leu Gln His Arg Thr Arg His Val Val Ala Pro Pro Gln Phe Gly Gly
145                     150                 )155                     160

Ser Gly Cys Pro Asn Leu Thr Glu Phe Gln Val Cys Gln Ser Ser Pro
                165                     170                     175

Cys Glu Ala Glu Glu Leu Arg Tyr Ser Leu His Val Gly Pro Trp Ser
                180                     185                     190

Thr Cys Ser Met Pro His Ser Arg Gln Val Arg Gln Ala Arg Arg Arg
        195                     200                     205

Gly Lys Asn Lys Glu Arg Glu Lys Asp Arg Ser Lys Gly Val Lys Asp
    210                     215                     220

Pro Glu Ala Arg Glu Leu Ile Lys Lys Lys Arg Asn Arg Asn Arg Gln
225                     230                     235                     240

Asn Arg Gln Glu Asn Lys Tyr Trp Asp Ile Gln Ile Gly Tyr Gln Thr
                245                     250                     255

Arg Glu Val Met Cys Ile Asn Lys Thr Gly Lys Ala Ala Asp Leu Ser
                260                     265                     270

Phe Cys Gln Gln Glu Lys Leu Pro Met Thr Phe Gln Ser Cys Val Ile
        275                     280                     285

Thr Lys Glu Cys Gln Val Ser Glu Trp Ser Glu Trp Ser Pro Cys Ser
    290                     295                     300

Lys Thr Cys His Asp Met Val Ser Pro Ala Gly Thr Arg Val Arg Thr
305                     310                     315                     320

Arg Thr Ile Arg Gln Phe Pro Ile Gly Ser Glu Lys Glu Cys Pro Glu
                325                     330                     335

Phe Glu Glu Lys Glu Pro Cys Leu Ser Gln Gly Asp Gly Val Val Pro
```

35

```
                 340                  345                     350

        Cys Ala Thr Tyr Gly Trp Arg Thr Thr Glu Trp Thr Glu Cys Arg Val
                 355                  360                  365

        Asp Pro Leu Leu Ser Gln Gln Asp Lys Arg Arg Gly Asn Gln Thr Ala
                 370                  375                  380

        Leu Cys Gly Gly Gly Ile Gln Thr Arg Glu Val Tyr Cys Val Gln Ala
        385                  390                  395                  400

        Asn Glu Asn Leu Leu Ser Gln Leu Ser Thr His Lys Asn Lys Glu Ala
                          405                  410                  415

        Ser Lys Pro Met Asp Leu Lys Leu Cys Thr Gly Pro Ile Pro Asn Thr
                 420                  425                  430

        Thr Gln Leu Cys His Ile Pro Cys Pro Thr Glu Cys Glu Val Ser Pro
                 435                  440                  445

        Trp Ser Ala Trp Gly Pro Cys Thr Tyr Glu Asn Cys Asn Asp Gln Gln
                 450                  455                  460

        Gly Lys Lys Gly Phe Lys Leu Arg Lys Arg Arg Ile Thr Asn Glu Pro
        465                  470                  475                  480

        Thr Gly Gly Ser Gly Val Thr Gly Asn Cys Pro His Leu Leu Glu Ala
                          485                  490                  495

        Ile Pro Cys Glu Glu Pro Ala Cys Tyr Asp Trp Lys Ala Val Arg Leu
                 500                  505                  510

        Gly Asp Cys Glu Pro Asp Asn Gly Lys Glu Cys Gly Pro Gly Thr Gln
                 515                  520                  525

        Val Gln Glu Val Val Cys Ile Asn Ser Asp Gly Glu Glu Val Asp Arg
                 530                  535                  540

        Gln Leu Cys Arg Asp Ala Ile Phe Pro Ile Pro Val Ala Cys Asp Ala
        545                  550                  555                  560

        Pro Cys Pro Lys Asp Cys Val Leu Ser Thr Trp Ser Thr Trp Ser Ser
                          565                  570                  575

        Cys Ser His Thr Cys Ser Gly Lys Thr Thr Glu Gly Lys Gln Ile Arg
                 580                  585                  590

        Ala Arg Ser Ile Leu Ala Tyr Ala Gly Glu Glu Gly Gly Ile Arg Cys
                 595                  600                  605

        Pro Asn Ser Ser Ala Leu Gln Glu Val Arg Ser Cys Asn Glu His Pro
                 610                  615                  620

        Cys Thr Val Tyr His Trp Gln Thr Gly Pro Trp Gly Gln Cys Ile Glu
        625                  630                  635                  640

        Asp Thr Ser Val Ser Ser Phe Asn Thr Thr Thr Trp Asn Gly Glu
```

36

```
                   645                   650                      655

Ala Ser Cys Ser Val Gly Met Gln Thr Arg Lys Val Ile Cys Val Arg
            660                   665                   670

Val Asn Val Gly Gln Val Gly Pro Lys Lys Cys Pro Glu Ser Leu Arg
            675                   680                   685

Pro Glu Thr Val Arg Pro Cys Leu Leu Pro Cys Lys Lys Asp Cys Ile
        690               695               700

Val Thr Pro Tyr Ser Asp Trp Thr Ser Cys Pro Ser Ser Cys Lys Glu
705               710               715                   720

Gly Asp Ser Ser Ile Arg Lys Gln Ser Arg His Arg Val Ile Ile Gln
                725                   730                   735

Leu Pro Ala Asn Gly Gly Arg Asp Cys Thr Asp Pro Leu Tyr Glu Glu
            740               745               750

Lys Ala Cys Glu Ala Pro Gln Ala Cys Gln Ser Tyr Arg Trp Lys Thr
        755               760               765

His Lys Trp Arg Arg Cys Gln Leu Val Pro Trp Ser Val Gln Gln Asp
    770               775               780

Ser Pro Gly Ala Gln Glu Gly Cys Gly Pro Gly Arg Gln Ala Arg Ala
785               790               795                   800

Ile Thr Cys Arg Lys Gln Asp Gly Gly Gln Ala Gly Ile His Glu Cys
            805               810               815

Leu Gln Tyr Ala Gly Pro Val Pro Ala Leu Thr Gln Ala Cys Gln Ile
            820               825               830

Pro Cys Gln Asp Asp Cys Gln Leu Thr Ser Trp Ser Lys Phe Ser Ser
        835               840               845

Cys Asn Gly Asp Cys Gly Ala Val Arg Thr Arg Lys Arg Thr Leu Val
    850               855               860

Gly Lys Ser Lys Lys Lys Glu Lys Cys Lys Asn Ser His Leu Tyr Pro
865               870               875                   880

Leu Ile Glu Thr Gln Tyr Cys Pro Cys Asp Lys Tyr Asn Ala Gln Pro
                885               890               895

Val Gly Asn Trp Ser Asp Cys Ile Leu Pro Glu Gly Lys Val Glu Val
            900               905               910

Leu Leu Gly Met Lys Val Gln Gly Asp Ile Lys Glu Cys Gly Gln Gly
            915               920               925

Tyr Arg Tyr Gln Ala Met Ala Cys Tyr Asp Gln Asn Gly Arg Leu Val
    930               935               940

Glu Thr Ser Arg Cys Asn Ser His Gly Tyr Ile Glu Glu Ala Cys Ile
```

37

```
945                    950                    955                    960
Ile Pro Cys Pro Ser Asp Cys Lys Leu Ser Glu Trp Ser Asn Trp Ser
              965                    970                    975

Arg Cys Ser Lys Ser Cys Gly Ser Gly Val Lys Val Arg Ser Lys Trp
              980                    985                    990

Leu Arg Glu Lys Pro Tyr Asn Gly Gly Arg Pro Cys Pro Lys Leu Asp
              995                   1000                   1005

His Val Asn Gln Ala Gln Val Tyr Glu Val Val Pro Cys His Ser Asp
     1010                   1015                   1020

Cys Asn Gln Tyr Leu Trp Val Thr Glu Pro Trp Ser Ile Cys Lys Val
1025                   1030                   1035                   1040

Thr Phe Val Asn Met Arg Glu Asn Cys Gly Glu Gly Val Gln Thr Arg
              1045                   1050                   1055

Lys Val Arg Cys Met Gln Asn Thr Ala Asp Gly Pro Ser Glu His Val
              1060                   1065                   1070

Glu Asp Tyr Leu Cys Asp Pro Glu Glu Met Pro Leu Gly Ser Arg Val
              1075                   1080                   1085

Cys Lys Leu Pro Cys Pro Glu Asp Cys Val Ile Ser Glu Trp Gly Pro
     1090                   1095                   1100

Trp Thr Gln Cys Val Leu Pro Cys Asn Gln Ser Ser Phe Arg Gln Arg
1105                   1110                   1115                   1120

Ser Ala Asp Pro Ile Arg Gln Pro Ala Asp Glu Gly Arg Ser Cys Pro
              1125                   1130                   1135

Asn Ala Val Glu Lys Glu Pro Cys Asn Leu Asn Lys Asn Cys Tyr His
              1140                   1145                   1150

Tyr Asp Tyr Asn Val Thr Asp Trp Ser Thr Cys Gln Leu Ser Glu Lys
     1155                   1160                   1165

Ala Val Cys Gly Asn Gly Ile Lys Thr Arg Met Leu Asp Cys Val Arg
     1170                   1175                   1180

Ser Asp Gly Lys Ser Val Asp Leu Lys Tyr Cys Glu Ala Leu Gly Leu
1185                   1190                   1195                   1200

Glu Lys Asn Trp Gln Met Asn Thr Ser Cys Met Val Glu Cys Pro Val
              1205                   1210                   1215

Asn Cys Gln Leu Ser Asp Trp Ser Pro Trp Ser Glu Cys Ser Gln Thr
              1220                   1225                   1230

Cys Gly Leu Thr Gly Lys Met Ile Arg Arg Arg Thr Val Thr Gln Pro
     1235                   1240                   1245

Phe Gln Gly Asp Gly Arg Pro Cys Pro Ser Leu Met Asp Gln Ser Lys
```

38

```
        1250                    1255                    1260

Pro Cys Pro Val Lys Pro Cys Tyr Arg Trp Gln Tyr Gly Gln Trp Ser
1265                    1270                    1275                    1280

Pro Cys Gln Val Gln Glu Ala Gln Cys Gly Glu Gly Thr Arg Thr Arg
                   1285                    1290                    1295

Asn Ile Ser Cys Val Val Ser Asp Gly Ser Ala Asp Asp Phe Ser Lys
              1300                    1305                    1310

Val Val Asp Glu Glu Phe Cys Ala Asp Ile Glu Leu Ile Ile Asp Gly
         1315                    1320                    1325

Asn Lys Asn Met Val Leu Glu Glu Ser Cys Ser Gln Pro Cys Pro Gly
    1330                    1335                    1340

Asp Cys Tyr Leu Lys Asp Trp Ser Ser Trp Ser Leu Cys Gln Leu Thr
1345                    1350                    1355                    1360

Cys Val Asn Gly Glu Asp Leu Gly Phe Gly Gly Ile Gln Val Arg Ser
              1365                    1370                    1375

Arg Pro Val Ile Ile Gln Glu Leu Glu Asn Gln His Leu Cys Pro Glu
         1380                    1385                    1390

Gln Met Leu Glu Thr Lys Ser Cys Tyr Asp Gly Gln Cys Tyr Glu Tyr
    1395                    1400                    1405

Lys Trp Met Ala Ser Ala Trp Lys Gly Ser Ser Arg Thr Val Trp Cys
   1410                    1415                    1420

Gln Arg Ser Asp Gly Ile Asn Val Thr Gly Gly Cys Leu Val Met Ser
1425                    1430                    1435                    1440

Gln Pro Asp Ala Asp Arg Ser Cys Asn Pro Pro Cys Ser Gln Pro His
              1445                    1450                    1455

Ser Tyr Cys Ser Glu Thr Lys Thr Cys His Cys Glu Glu Gly Tyr Thr
              1460                    1465                    1470

Glu Val Met Ser Ser Asn Ser Thr Leu Glu Gln Cys Thr Leu Ile Pro
    1475                    1480                    1485

Val Val Val Leu Pro Thr Met Glu Asp Lys Arg Gly Asp Val Lys Thr
    1490                    1495                    1500

Ser Arg Ala Val His Pro Thr Gln Pro Ser Ser Asn Pro Ala Gly Arg
1505                    1510                    1515                    1520

Gly Arg Thr Trp Phe Leu Gln Pro Phe Gly Pro Asp Gly Arg Leu Lys
              1525                    1530                    1535

Thr Trp Val Tyr Gly Val Ala Ala Gly Ala Phe Val Leu Leu Ile Phe
              1540                    1545                    1550

Ile Val Ser Met Ile Tyr Leu Ala Cys Lys Lys Pro Lys Lys Pro Gln
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Arg Arg Gln Asn Asn Arg Leu Lys Pro Leu Thr Leu Ala Tyr Asp Gly
  1570   1575   1580

Asp Ala Asp Met
1585

<210> 42
<211> 1447
<212> DNA
<213> human

<400> 42
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ataaatt 1447

<210> 43
<211> 224
<212> PRT
<213> human

<400> 43
Met Ser Asp Glu Asp Ser Cys Val Ala Cys Gly Ser Leu Arg Thr Ala
  1   5   10   15

Gly Pro Gln Ala Gly Ala Pro Ser Pro Trp Pro Trp Glu Ala Arg Leu
          20   25   30

Met His Gln Gly Gln Leu Ala Cys Gly Gly Ala Leu Val Ser Glu Glu
         35   40   45

```
Ala Val Leu Thr Ala Ala His Cys Phe Ile Gly Arg Gln Ala Pro Glu
    50                  55                  60

Glu Trp Ser Val Gly Leu Gly Thr Arg Pro Glu Glu Trp Gly Leu Lys
 65                  70                  75                  80

Gln Leu Ile Leu His Gly Ala Tyr Thr His Pro Glu Gly Gly Tyr Asp
                    85                  90                  95

Met Ala Leu Leu Leu Leu Ala Gln Pro Val Thr Leu Gly Ala Ser Leu
                100                 105                 110

Arg Pro Leu Cys Leu Pro Tyr Ala Asp His His Leu Pro Asp Gly Glu
            115                 120                 125

Arg Gly Trp Val Leu Gly Arg Ala Arg Pro Gly Ala Gly Ile Ser Ser
    130                 135                 140

Leu Gln Thr Val Pro Val Thr Leu Leu Gly Pro Arg Ala Cys Ser Arg
145                 150                 155                 160

Leu His Ala Ala Pro Gly Gly Asp Gly Ser Pro Ile Leu Pro Gly Met
                165                 170                 175

Val Cys Thr Ser Ala Val Gly Glu Leu Pro Ser Cys Glu Ala Asn Gln
                180                 185                 190

Pro Ala Ala Asp Arg Gly Pro Gly His Ser Gln Glu Gln Glu Asn Ala
            195                 200                 205

Gly Arg Gln Met Ala Leu Leu Pro Leu Ser Ser Pro Pro Cys His Val
    210                 215                 220
```

<210> 44
<211> 1592
<212> DNA
<213> human

<400> 44
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cgccccacat gtaactgtat ctacaaccag ctgcaccagc gacacctgtc caacccggcc 660
cggcctggga tgctatgtgg gggcccccag cctggggtgc agggcccctg tcaggagat 720
tccgggggcc ctgtgctgtg cctcgagcct gacggacact gggttcaggc tggcatcatc 780
agctttgcat caagctgtgc ccaggaggac gctcctgtgc tgctgaccaa cacagctgct 840
```

41

```
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tcctcccac cctgtcatgt gtgattccag gc                                1592
```

<210> 45
<211> 521
<212> PRT
<213> human

<400> 45

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Met Leu Leu Ser Ser Leu Val Ser Leu Ala Gly Ser Val Tyr Leu Ala
 1               5                  10                  15

Trp Ile Leu Phe Phe Val Leu Tyr Asp Phe Cys Ile Val Cys Ile Thr
            20                  25                  30

Thr Tyr Ala Ile Asn Val Ser Leu Met Trp Leu Ser Phe Arg Lys Val
        35                  40                  45

Gln Glu Pro Gln Gly Gln Pro Lys Pro Gln Glu Gly Asn Thr Val Pro
    50                  55                  60

Gly Glu Trp Pro Trp Gln Ala Ser Val Arg Arg Gln Gly Ala His Ile
65                  70                  75                  80

Cys Ser Gly Ser Leu Val Ala Asp Thr Trp Val Leu Thr Ala Ala His
                85                  90                  95

Cys Phe Glu Lys Ala Ala Ala Thr Glu Leu Asn Ser Cys Val Arg Asp
            100                 105                 110

Ser Ala Pro Gly Ala Glu Glu Val Gly Val Ala Ala Leu Gln Leu Pro
            115                 120                 125

Arg Ala Tyr Asn His Tyr Ser Gln Gly Ser Asp Leu Ala Leu Leu Gln
    130                 135                 140

Leu Ala His Pro Thr Thr His Thr Pro Leu Cys Leu Pro Gln Pro Ala
145                 150                 155                 160

His Arg Phe Pro Phe Gly Ala Ser Cys Trp Ala Thr Gly Trp Asp Gln
            165                 170                 175

Asp Thr Ser Asp Ala Pro Gly Thr Leu Arg Asn Leu Arg Leu Arg Leu
            180                 185                 190
```

42

```
Ile Ser Arg Pro Thr Cys Asn Cys Ile Tyr Asn Gln Leu His Gln Arg
    195                 200             205

His Leu Ser Asn Pro Ala Arg Pro Gly Met Leu Cys Gly Gly Pro Gln
    210             215             220

Pro Gly Val Gln Gly Pro Cys Gln Gly Asp Ser Gly Gly Pro Val Leu
225             230             235                 240

Cys Leu Glu Pro Asp Gly His Trp Val Gln Ala Gly Ile Ile Ser Phe
            245             250             255

Ala Ser Ser Cys Ala Gln Glu Asp Ala Pro Val Leu Leu Thr Asn Thr
            260             265             270

Ala Ala His Ser Ser Trp Leu Gln Ala Arg Val Gln Gly Ala Ala Phe
        275             280             285

Leu Ala Gln Ser Pro Glu Thr Pro Glu Met Ser Asp Glu Asp Ser Cys
    290             295             300

Val Ala Cys Gly Ser Leu Arg Thr Ala Gly Pro Gln Ala Gly Ala Pro
305             310             315             320

Ser Pro Trp Pro Trp Glu Ala Arg Leu Met His Gln Gly Gln Leu Ala
            325             330             335

Cys Gly Gly Ala Leu Val Ser Glu Glu Ala Val Leu Thr Ala Ala His
            340             345             350

Cys Phe Ile Gly Arg Gln Ala Pro Glu Glu Trp Ser Val Gly Leu Gly
        355             360             365

Thr Arg Pro Glu Glu Trp Gly Leu Lys Gln Leu Ile Leu His Gly Ala
    370             375             380

Tyr Thr His Pro Glu Gly Gly Tyr Asp Met Ala Leu Leu Leu Leu Ala
385             390             395             400

Gln Pro Val Thr Leu Gly Ala Ser Leu Arg Pro Leu Cys Leu Pro Tyr
            405             410             415

Ala Asp His His Leu Pro Asp Gly Glu Arg Gly Trp Val Leu Gly Arg
        420             425             430

Ala Arg Pro Gly Ala Gly Ile Ser Ser Leu Gln Thr Val Pro Val Thr
        435             440             445

Leu Leu Gly Pro Arg Ala Cys Ser Arg Leu His Ala Ala Pro Gly Gly
    450             455             460

Asp Gly Ser Pro Ile Leu Pro Gly Met Val Cys Thr Ser Ala Val Gly
465             470             475             480

Glu Leu Pro Ser Cys Glu Ala Asn Gln Pro Ala Ala Asp Arg Gly Pro
            485             490             495
```

43

Gly His Ser Gln Glu Gln Glu Asn Ala Gly Arg Gln Met Ala Leu Leu
            500   505   510

Pro Leu Ser Ser Pro Pro Cys His Val
        515   520

<210> 46
<211> 1200
<212> DNA
<213> human

<400> 46
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actgggttca ggctggcatc atcagctttg catcaagctg tgcccaggag gacgctcctg 180
tgctgctgac caacacagct gctcacagtt cctggctgca ggctcgagtt caggggggcag 240
ctttcctggc ccagagccca gagaccccgg agatgagtga tgaggacagc tgtgtagcct 300
gtggatcctt gaggacagca ggtccccagg caggagcacc ctccccatgg ccctgggagg 360
ccaggctgat gcaccaggga cagctggcct gtggcggagc cctggtgtca gaggaggcgg 420
tgctaactgc tgcccactgc ttcattgggc gccaggcccc agaggaatgg agcgtagggc 480
tggggaccag accggaggag tggggcctga agcagctcat cctgcatgga gcctacaccc 540
accctgaggg gggctacgac atggccctcc tgctgctggc ccagcctgtg acactgggag 600
ccagcctgcg gcccctctgc ctgccctatg ctgaccacca cctgcctgat ggggagcgtg 660
gctgggttct gggacgggcc cgcccaggag caggcatcag ctccctccag acagtgcccg 720
tgaccctcct ggggcctagg gcctgcagcc ggctgcatgc agctcctggg ggtgatggca 780
gccctattct gccggggatg gtgtgtacca gtgctgtggg tgagctgccc agctgtgagg 840
ccaaccaacc agctgctgac aggggacctg gccattctca ggaacaagag aatgcaggca 900
ggcaaatggc attactgccc ctgtcctccc cacccctgtca tgtgtgattc caggcaccag 960
ggcaggccca gaagcccagc agctgtggga aggaacctgc ctggggccac aggtgcccac 1020
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caggcgtctc agctttcctc ctcctttacc ctttcagata caatcacgcc agccacgttg 1140
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<210> 47
<211> 304
<212> PRT
<213> human

<400> 47
Met Leu Cys Gly Gly Pro Gln Pro Gly Val Gln Gly Pro Cys Gln Gly
  1   5   10   15

Asp Ser Gly Gly Pro Val Leu Cys Leu Glu Pro Asp Gly His Trp Val
            20   25   30

Gln Ala Gly Ile Ile Ser Phe Ala Ser Ser Cys Ala Gln Glu Asp Ala
            35   40   45

Pro Val Leu Leu Thr Asn Thr Ala Ala His Ser Ser Trp Leu Gln Ala
      50   55   60

Arg Val Gln Gly Ala Ala Phe Leu Ala Gln Ser Pro Glu Thr Pro Glu
  65   70   75   80

Met Ser Asp Glu Asp Ser Cys Val Ala Cys Gly Ser Leu Arg Thr Ala

```
                    85                      90                      95

Gly Pro Gln Ala Gly Ala Pro Ser Pro Trp Pro Trp Glu Ala Arg Leu
            100                 105                 110

Met His Gln Gly Gln Leu Ala Cys Gly Gly Ala Leu Val Ser Glu Glu
            115                 120                 125

Ala Val Leu Thr Ala Ala His Cys Phe Ile Gly Arg Gln Ala Pro Glu
            130                 135                 140

Glu Trp Ser Val Gly Leu Gly Thr Arg Pro Glu Glu Trp Gly Leu Lys
145                 150                 155                 160

Gln Leu Ile Leu His Gly Ala Tyr Thr His Pro Glu Gly Gly Tyr Asp
                    165                 170                 175

Met Ala Leu Leu Leu Leu Ala Gln Pro Val Thr Leu Gly Ala Ser Leu
            180                 185                 190

Arg Pro Leu Cys Leu Pro Tyr Ala Asp His His Leu Pro Asp Gly Glu
            195                 200                 205

Arg Gly Trp Val Leu Gly Arg Ala Arg Pro Gly Ala Gly Ile Ser Ser
            210                 215                 220

Leu Gln Thr Val Pro Val Thr Leu Leu Gly Pro Arg Ala Cys Ser Arg
225                 230                 235                 240

Leu His Ala Ala Pro Gly Gly Asp Gly Ser Pro Ile Leu Pro Gly Met
                    245                 250                 255

Val Cys Thr Ser Ala Val Gly Glu Leu Pro Ser Cys Glu Ala Asn Gln
            260                 265                 270

Pro Ala Ala Asp Arg Gly Pro Gly His Ser Gln Glu Gln Glu Asn Ala
            275                 280                 285

Gly Arg Gln Met Ala Leu Leu Pro Leu Ser Ser Pro Pro Cys His Val
    290                 295                 300
```

<210> 48
<211> 1214
<212> DNA
<213> human

<400> 48
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gggcagcgcc cccggacgtc tgccccctcc cgcgccggtg ccctgctgct gctgcttctg 120
ttgctgaggt ctgcaggttg ctggggcgca ggggaagccc cggggggcgct gtccactgct 180
gatcccgccg accagagcgt ccagtgtgtc cccaaggcca cctgtccttc cagccggcct 240
cgccttctct ggcagacccc gaccacccag acactgccct cgaccaccat ggagacccaa 300
ttcccagttt ctgaaggcaa agtcgaccca taccgctcct gtggcttttc ctacgagcag 360
```

```
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cgggccaatg gcacacacat ctgtgccggc accatcattg cctcccagtg ggtgctgact 480
gtggcccact gcctgatctg gcgtgatgtt atctactcag tgagggtggg gagtccgtgg 540
attgaccaga tgacgcagac cgcctccgat gtcccggtgc tccaggtcat catgcatagc 600
aggtaccggg cccagcggtt ctggtcctgg gtgggccagg ccaacgacat cggcctcctc 660
aagctcaagc aggaactcaa gtacagcaat tacgtgcggc ccatctgcct gcctggcacg 720
gactatgtgt tgaaggacca ttcccgctgc actgtgacgg ctgggggact ttccaaggct 780
gacggcatgt ggcctcagtt ccggaccatt caggagaagg aagtcatcat cctgaacaac 840
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cactggatct gggactgcct caacgggcag gccctggccc tgccagcccc atccaggacc 1140
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tccctcactt gtga                                                  1214
```

```
Met Gly Arg Trp Cys Gln Thr Val Ala Arg Gly Gln Arg Pro Arg Thr
 1               5                  10                  15

Ser Ala Pro Ser Arg Ala Gly Ala Leu Leu Leu Leu Leu Leu Leu
            20              25                  30

Arg Ser Ala Gly Cys Trp Gly Ala Gly Glu Ala Pro Gly Ala Leu Ser
        35                  40                  45

Thr Ala Asp Pro Ala Asp Gln Ser Val Gln Cys Val Pro Lys Ala Thr
    50                  55                  60

Cys Pro Ser Ser Arg Pro Arg Leu Leu Trp Gln Thr Pro Thr Thr Gln
 65                  70                  75                  80

Thr Leu Pro Ser Thr Thr Met Glu Thr Gln Phe Pro Val Ser Glu Gly
                85                  90                  95

Lys Val Asp Pro Tyr Arg Ser Cys Gly Phe Ser Tyr Glu Gln Asp Pro
            100                 105                 110

Thr Leu Arg Asp Pro Glu Ala Val Ala Arg Arg Trp Pro Trp Met Val
            115                 120                 125

Ser Val Arg Ala Asn Gly Thr His Ile Cys Ala Gly Thr Ile Ile Ala
    130                 135                 140

Ser Gln Trp Val Leu Thr Val Ala His Cys Leu Ile Trp Arg Asp Val
145                 150                 155                 160

Ile Tyr Ser Val Arg Val Gly Ser Pro Trp Ile Asp Gln Met Thr Gln
                165                 170                 175

Thr Ala Ser Asp Val Pro Val Leu Gln Val Ile Met His Ser Arg Tyr
```

```
              180                 185                  190

Arg Ala Gln Arg Phe Trp Ser Trp Val Gly Gln Ala Asn Asp Ile Gly
        195                 200                 205

Leu Leu Lys Leu Lys Gln Glu Leu Lys Tyr Ser Asn Tyr Val Arg Pro
        210                 215                 220

Ile Cys Leu Pro Gly Thr Asp Tyr Val Leu Lys Asp His Ser Arg Cys
225                 230                 235                 240

Thr Val Thr Gly Trp Gly Leu Ser Lys Ala Asp Gly Met Trp Pro Gln
            245                 250                 255

Phe Arg Thr Ile Gln Glu Lys Glu Val Ile Ile Leu Asn Asn Lys Glu
        260                 265                 270

Cys Asp Asn Phe Tyr His Asn Phe Thr Lys Ile Pro Thr Leu Val Gln
        275                 280                 285

Ile Ile Lys Ser Gln Met Met Cys Ala Glu Asp Thr His Arg Glu Lys
    290                 295                 300

Phe Cys Tyr Glu Leu Thr Gly Glu Pro Leu Val Cys Ser Met Glu Gly
305                 310                 315                 320

Thr Trp Tyr Leu Val Gly Leu Val Ser Trp Gly Ala Gly Cys Gln Lys
            325                 330                 335

Ser Glu Ala Pro Pro Ile Tyr Leu Gln Val Ser Ser Tyr Gln His Trp
            340                 345                 350

Ile Trp Asp Cys Leu Asn Gly Gln Ala Leu Ala Leu Pro Ala Pro Ser
        355                 360                 365

Arg Thr Leu Leu Leu Ala Leu Pro Leu Pro Leu Ser Leu Leu Ala Ala
        370                 375                 380

Leu
385


<210> 50
<211> 937
<212> DNA
<213> human

<400> 50
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tccccgaatc cccgctccca ggctacctaa gaggatgagc ggtgctccga cggccggggc 180
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47

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cctggagaag cagcacctgc gaattcagca tctgcaaagc cagtttggcc tcctggacca 600
caagcaccta gaccatgagg tggccaagcc tgcccgaaga aagaggctgc ccgagatggc 660
ccagccagtt gacccggctc acaatgtcag ccgcctgcac cgaggctggt ggtttggcac 720
ctgcagccat tccaacctca acggccagta cttccgctcc atcccacagc agcggcagaa 780
gcttaagaag ggaatcttct ggaagaacctg gcggggccgc tactacccgc tgcaggcac 840
caccatgttg atccagccca tggcagcaga ggcagcctcc tagcgtcctg gctgggcctg 900
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<210> 51
<211> 242
<212> PRT
<213> human

<400> 51

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Met Ser Gly Ala Pro Thr Ala Gly Ala Ala Leu Met Leu Cys Ala Ala
1               5                   10                  15

Thr Ala Val Leu Leu Ser Ala Arg Ser Gly Pro Val Gln Ser Lys Ser
            20                  25                  30

Pro Arg Phe Ala Ser Trp Asp Glu Met Asn Val Leu Ala His Gly Leu
        35                  40                  45

Leu Gln Leu Gly Gln Gly Leu Arg Glu His Ala Glu Arg Thr Arg Ser
    50                  55                  60

Gln Leu Ser Ala Leu Glu Arg Arg Leu Ser Ala Cys Gly Ser Ala Cys
65                  70                  75                  80

Gln Gly Thr Glu Gly Ser Thr Asp Leu Pro Leu Ala Pro Glu Ser Arg
                85                  90                  95

Val Asp Pro Glu Val Leu His Ser Leu Gln Thr Gln Leu Lys Ala Gln
            100                 105                 110

Asn Ser Arg Ile Gln Gln Leu Phe His Lys Val Ala Gln Gln Gln Arg
            115                 120                 125

His Leu Glu Lys Gln His Leu Arg Ile Gln His Leu Gln Ser Gln Phe
    130                 135                 140

Gly Leu Leu Asp His Lys His Leu Asp His Glu Val Ala Lys Pro Ala
145                 150                 155                 160

Arg Arg Lys Arg Leu Pro Glu Met Ala Gln Pro Val Asp Pro Ala His
                165                 170                 175

Asn Val Ser Arg Leu His Arg Gly Trp Trp Phe Gly Thr Cys Ser His
            180                 185                 190

Ser Asn Leu Asn Gly Gln Tyr Phe Arg Ser Ile Pro Gln Gln Arg Gln
            195                 200                 205

Lys Leu Lys Lys Gly Ile Phe Trp Lys Thr Trp Arg Gly Arg Tyr Tyr
    210                 215                 220
```

48

Pro Leu Gln Ala Thr Thr Met Leu Ile Gln Pro Met Ala Ala Glu Ala
225   230   235   240

Ala Ser

<210> 52
<211> 1239
<212> DNA
<213> human

<400> 52
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ctttgcgtcc tgggacgaga tgaatgtcct ggcgcacgga ctcctgcagc tcggccaggg 240
gctgcgcgaa cacgcggagc gcacccgcag tcagctgagc gcgctggagc ggcgcctgag 300
cgcgtgcggg tccgcctgtc agggaaccga ggggtccacc gacctcccgt tagcccctga 360
gagccgggtg gaccctgagg tccttcacag cctgcagaca caactcaagg ctcagaacag 420
caggatccag caactcttcc acaaggtggc ccagcagcag cggcacctgg agaagcagca 480
cctgcgaatt cagcatctgc aaagccagtt tggcctcctg gaccacaagc acctagacca 540
tgagggtggc aagcctgccc gaagaaagag gctgcccgag atggcccagc cagttgaccc 600
ggctcacaat gtcagccgcc tgcaccatgg aggctggaca gtaattcaga ggcgccacga 660
tggctcagtg gacttcaacc ggccctggga agcctacaag gcggggtttg gggatcccca 720
cggcgagttc tggctgggtc tggagaaggt gcatagcatc atggggggacc gcaacagccg 780
cctggccgtg cagctgcggg actgggatgg caacgccgag ttgctgcagt ctccgtgca 840
cctgggtggc gaggacacgg cctatagcct gcagctcact gcaccgtgg ccggccagct 900
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cacctgcagc cattccaacc tcaacggcca gtacttccgc tccatcccac agcagcggca 1080
gaagcttaag aagggaatct tctggaagac ctggcggggc cgctactacc cgctgcaggc 1140
caccaccatg ttgatccagc ccatggcagc agaggcagcc tcctagcgtc ctggctgggc 1200
ctggtcccag gcccacgaaa gaggtgactc ttggctctg   1239

<210> 53
<211> 368
<212> PRT
<213> human

<400> 53
Met Ser Gly Ala Pro Thr Ala Gly Ala Ala Leu Met Leu Cys Ala Ala
 1   5   10   15

Thr Ala Val Leu Leu Ser Ala Gln Gly Gly Pro Val Gln Ser Lys Ser
             20   25   30

Pro Arg Phe Ala Ser Trp Asp Glu Met Asn Val Leu Ala His Gly Leu
         35   40   45

Leu Gln Leu Gly Gln Gly Leu Arg Glu His Ala Glu Arg Thr Arg Ser
     50   55   60

Gln Leu Ser Ala Leu Glu Arg Arg Leu Ser Ala Cys Gly Ser Ala Cys
 65   70   75   80

49

```
Gln Gly Thr Glu Gly Ser Thr Asp Leu Pro Leu Ala Pro Glu Ser Arg
                85                  90                  95

Val Asp Pro Glu Val Leu His Ser Leu Gln Thr Gln Leu Lys Ala Gln
            100                 105                 110

Asn Ser Arg Ile Gln Gln Leu Phe His Lys Val Ala Gln Gln Gln Arg
            115                 120                 125

His Leu Glu Lys Gln His Leu Arg Ile Gln His Leu Gln Ser Gln Phe
            130                 135                 140

Gly Leu Leu Asp His Lys His Leu Asp His Glu Gly Gly Lys Pro Ala
145                 150                 155                 160

Arg Arg Lys Arg Leu Pro Glu Met Ala Gln Pro Val Asp Pro Ala His
                165                 170                 175

Asn Val Ser Arg Leu His His Gly Gly Trp Thr Val Ile Gln Arg Arg
            180                 185                 190

His Asp Gly Ser Val Asp Phe Asn Arg Pro Trp Glu Ala Tyr Lys Ala
            195                 200                 205

Gly Phe Gly Asp Pro His Gly Glu Phe Trp Leu Gly Leu Glu Lys Val
210                 215                 220

His Ser Ile Met Gly Asp Arg Asn Ser Arg Leu Ala Val Gln Leu Arg
225                 230                 235                 240

Asp Trp Asp Gly Asn Ala Glu Leu Leu Gln Phe Ser Val His Leu Gly
                245                 250                 255

Gly Glu Asp Thr Ala Tyr Ser Leu Gln Leu Thr Ala Pro Val Ala Gly
            260                 265                 270

Gln Leu Gly Ala Thr Thr Val Pro Pro Ser Gly Leu Ser Val Pro Phe
            275                 280                 285

Ser Thr Trp Asp Gln Asp His Asp Leu Arg Arg Asp Lys Asn Cys Ala
    290                 295                 300

Lys Ser Leu Ser Gly Gly Trp Trp Phe Gly Thr Cys Ser His Ser Asn
305                 310                 315                 320

Leu Asn Gly Gln Tyr Phe Arg Ser Ile Pro Gln Gln Arg Gln Lys Leu
            325                 330                 335

Lys Lys Gly Ile Phe Trp Lys Thr Trp Arg Gly Arg Tyr Tyr Pro Leu
            340                 345                 350

Gln Ala Thr Thr Met Leu Ile Gln Pro Met Ala Ala Glu Ala Ala Ser
    355                 360                 365
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50

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<212> DNA
<213> human

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<213> human

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Thr Ala Val Leu Leu Ser Ala Arg Ser Gly Pro Val Gln Ser Lys Ser
            20   25   30

Pro Arg Phe Ala Ser Trp Asp Glu Met Asn Val Leu Ala His Gly Leu
        35   40   45

Leu Gln Leu Gly Gln Gly Leu Arg Glu His Ala Glu Arg Thr Arg Ser
    50   55   60

Gln Leu Ser Ala Leu Glu Arg Arg Leu Ser Ala Cys Gly Ser Ala Cys
65   70   75   80

Gln Gly Thr Glu Gly Ser Thr Asp Leu Pro Leu Ala Pro Glu Ser Arg
                85   90   95

Val Asp Pro Glu Val Leu His Ser Leu Gln Thr Gln Leu Lys Ala Gln
            100   105   110

51

```
Asn Ser Arg Ile Gln Gln Leu Phe His Lys Val Ala Gln Gln Gln Arg
        115             120             125

His Leu Glu Lys Gln His Leu Arg Ile Gln His Leu Gln Ser Gln Phe
    130             135             140

Gly Leu Leu Asp His Lys His Leu Asp His Glu Val Ala Lys Pro Ala
145             150             155             160

Arg Arg Lys Arg Leu Pro Glu Met Ala Gln Pro Val Asp Pro Ala His
            165             170             175

Asn Val Ser Arg Leu His His Gly Gly Trp Thr Val Ile Gln Arg Arg
            180             185             190

His Asp Gly Ser Met Asp Phe Asn Arg Pro Trp Glu Ala Tyr Lys Ala
        195             200             205

Gly Phe Gly Asp Pro His Gly Glu Phe Trp Leu Gly Leu Glu Lys Val
    210             215             220

His Ser Ile Thr Gly Asp Arg Asn Ser Arg Leu Ala Val Gln Leu Arg
225             230             235             240

Asp Trp Asp Gly Asn Ala Glu Leu Leu Gln Phe Ser Val His Leu Gly
            245             250             255

Gly Glu Asp Thr Ala Tyr Ser Leu Gln Leu Thr Ala Pro Val Ala Gly
        260             265             270

Gln Leu Gly Ala Thr Thr Val Pro Pro Ser Gly Leu Ser Val Pro Phe
        275             280             285

Ser Thr Trp Asp Gln Asp His Asp Leu Arg Arg Asp Lys Asn Cys Ala
    290             295             300

Lys Ser Leu Ser Ala Pro Ser Val Ala Gln Arg Pro Asp His Val Pro
305             310             315             320

Ser Pro Leu Thr Pro Ala Gly Gly Trp Trp Phe Gly Thr Cys Ser His
            325             330             335

Ser Asn Leu Asn Gly Gln Tyr Phe Arg Ser Ile Pro Gln Gln Arg Gln
            340             345             350

Lys Leu Lys Lys Gly Ile Phe Trp Lys Thr Trp Arg Gly Arg Tyr Tyr
            355             360             365

Pro Leu Gln Ala Thr Thr Met Leu Ile Gln Pro Met Ala Ala Glu Ala
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Ala Ser
385


<210> 56
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52

<211> 1150
<212> DNA
<213> human

<400> 56
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<210> 57
<211> 368
<212> PRT
<213> human

<400> 57
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1               5                   10                  15

Thr Ala Val Leu Leu Ser Ala Gln Gly Gly Pro Val Gln Ser Lys Ser
            20                  25                  30

Pro Arg Phe Ala Ser Trp Asp Glu Met Asn Val Leu Ala His Gly Leu
        35                  40                  45

Leu Gln Leu Gly Gln Gly Leu Arg Glu His Ala Glu Arg Thr Arg Ser
    50                  55                  60

Gln Leu Ser Ala Leu Glu Arg Arg Leu Ser Ala Cys Gly Ser Ala Cys
65                  70                  75                  80

Gln Gly Thr Glu Gly Ser Thr Asp Leu Pro Leu Ala Pro Glu Ser Arg
                85                  90                  95

Val Asp Pro Glu Val Leu His Ser Leu Gln Thr Gln Leu Lys Ala Gln
            100                 105                 110

Asn Ser Arg Ile Gln Gln Leu Phe His Lys Val Ala Gln Gln Gln Arg
        115                 120                 125
```

53

```
His Leu Glu Lys Gln His Leu Arg Ile Gln His Leu Gln Ser Gln Phe
    130             135             140

Gly Leu Leu Asp His Lys His Leu Asp His Glu Val Ala Lys Pro Ala
145             150             155             160

Arg Arg Lys Arg Leu Pro Glu Met Ala Gln Pro Val Asp Pro Ala His
            165             170             175

Asn Val Ser Arg Leu His His Gly Gly Trp Thr Val Ile Gln Arg Arg
            180             185             190

His Asp Gly Ser Val Asp Phe Asn Arg Pro Trp Glu Ala Tyr Lys Ala
            195             200             205

Gly Phe Gly Asp Pro His Gly Glu Phe Trp Leu Gly Leu Glu Lys Val
    210             215             220

His Ser Ile Thr Gly Asp Arg Asn Ser Arg Leu Ala Val Gln Leu Arg
225             230             235             240

Asp Trp Asp Asp Asn Ala Glu Leu Leu Gln Phe Ser Val His Leu Gly
            245             250             255

Gly Glu Asp Thr Ala Tyr Ser Leu Gln Leu Thr Ala Pro Val Ala Gly
            260             265             270

Gln Leu Gly Ala Thr Thr Val Pro Pro Ser Gly Leu Ser Val Pro Phe
            275             280             285

Pro Thr Trp Asp Gln Asp His Asp Leu Arg Arg Asp Lys Asn Cys Ala
    290             295             300

Lys Ser Leu Ser Gly Gly Trp Trp Phe Gly Thr Cys Ser His Ser Asn
305             310             315             320

Leu Asn Gly Gln Tyr Phe Arg Ser Ile Pro Gln Gln Arg Gln Lys Leu
            325             330             335

Lys Lys Gly Ile Phe Trp Lys Thr Trp Arg Gly Arg Tyr Tyr Pro Leu
            340             345             350

Gln Ala Thr Thr Met Leu Ile Gln Pro Met Ala Ala Glu Ala Ala Ser
    355             360             365
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<211> 6373
<212> DNA
<213> human

<220>
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54

<223> Wherein N is A, or T, or C, or G.

<400> 58
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<211> 5669

<400> 59

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<211> 1661
<212> DNA
<213> human

<400> 60
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<210> 61
<211> 501
<212> PRT
<213> human

<400> 61

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Ile Cys Ser Gly Ser Leu Val Ala Asp Thr Trp Val Leu Thr Ala Ala
                20                  25                  30

His Cys Phe Glu Lys Ala Ala Ala Thr Glu Leu Asn Ser Trp Ser Val
            35                  40                  45

Val Leu Gly Ser Leu Gln Arg Glu Gly Leu Ser Pro Gly Ala Glu Glu
        50                  55                  60

Val Gly Val Ala Ala Leu Gln Leu Pro Arg Ala Tyr Asn His Tyr Ser
65                  70                  75                  80

Gln Gly Ser Asp Leu Ala Leu Leu Gln Leu Ala His Pro Thr Thr His
                85                  90                  95

Thr Pro Leu Cys Leu Pro Gln Pro Ala His Arg Phe Pro Phe Gly Ala
                100                 105                 110

Ser Cys Trp Ala Thr Gly Trp Asp Gln Asp Thr Ser Asp Ala Pro Gly
            115                 120                 125

Thr Leu Arg Asn Leu Arg Leu Arg Leu Ile Ser Arg Pro Thr Cys Asn
        130                 135                 140

Cys Ile Tyr Asn Gln Leu His Gln Arg His Leu Ser Asn Pro Ala Arg
```

```
         145                      150                      155                      160
```

Pro Gly Met Leu Cys Gly Gly Pro Gln Pro Gly Val Gln Gly Pro Cys
                165   170   175

Gln Gly Asp Ser Gly Gly Pro Val Leu Cys Leu Glu Pro Asp Gly His
                180   185   190

Trp Val Gln Ala Gly Ile Ile Ser Phe Ala Ser Ser Cys Ala Gln Glu
                195   200   205

Asp Ala Pro Val Leu Leu Thr Asn Thr Ala Ala His Ser Ser Trp Leu
     210   215   220

Gln Ala Arg Val Gln Gly Ala Ala Phe Leu Ala Gln Ser Pro Glu Thr
225   230   235   240

Pro Glu Met Ser Asp Glu Asp Ser Cys Val Ala Cys Gly Ser Leu Arg
                245   250   255

Thr Ala Gly Pro Gln Ala Gly Ala Pro Ser Pro Trp Pro Trp Glu Ala
                260   265   270

Arg Leu Met His Gln Gly Gln Leu Ala Cys Gly Gly Ala Leu Val Ser
                275   280   285

Glu Glu Ala Val Leu Thr Ala Ala His Cys Phe Ile Gly Arg Gln Ala
     290   295   300

Pro Glu Glu Trp Ser Val Gly Leu Gly Thr Arg Pro Glu Glu Trp Gly
305   310   315   320

Leu Lys Gln Leu Ile Leu His Gly Ala Tyr Thr His Pro Glu Gly Gly
                325   330   335

Tyr Asp Met Ala Leu Leu Leu Leu Ala Gln Pro Val Thr Leu Gly Ala
                340   345   350

Ser Leu Arg Pro Leu Cys Leu Pro Tyr Pro Asp His His Leu Pro Asp
                355   360   365

Gly Glu Arg Gly Trp Val Leu Gly Arg Ala Arg Pro Gly Ala Gly Ile
     370   375   380

Ser Ser Leu Gln Thr Val Pro Val Thr Leu Leu Gly Pro Arg Ala Cys
385   390   395   400

Ser Arg Leu His Ala Ala Pro Gly Gly Asp Gly Ser Pro Ile Leu Pro
                405   410   415

Gly Met Val Cys Thr Ser Ala Val Gly Glu Leu Pro Ser Cys Glu Gly
                420   425   430

Leu Ser Gly Ala Pro Leu Val His Glu Val Arg Gly Thr Trp Phe Leu
                435   440   445

Ala Gly Leu His Ser Phe Gly Asp Ala Cys Gln Gly Pro Ala Arg Pro

```
                450                    455                    460

Ala Val Phe Thr Ala Leu Pro Ala Tyr Glu Asp Trp Val Ser Ser Leu
465                   470                    475                  480

Asp Trp Gln Val Tyr Phe Ala Glu Glu Pro Glu Pro Glu Ala Glu Pro
                  485                    490                    495

Gly Ser Cys Leu Ala
              500
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<210> 62
<211> 342
<212> DNA
<213> human

<400> 62
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<210> 63
<211> 1139
<212> DNA
<213> human

<400> 63
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<210> 64
<211> 768
<212> DNA
<213> human

<400> 64
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<210> 65
<211> 493
<212> PRT
<213> human

<400> 65
Met Leu Leu Ser Ser Leu Val Ser Leu Ala Gly Ser Val Tyr Leu Ala
 1   5   10   15

Trp Ile Leu Phe Phe Val Leu Tyr Asp Phe Cys Ile Val Cys Ile Thr
                20   25   30

Thr Tyr Ala Ile Asn Val Ser Leu Met Trp Leu Ser Phe Arg Lys Val
            35   40   45

Gln Glu Pro Gln Gly Lys Ala Lys Arg His Gly Asn Thr Val Pro Gly
        50   55   60

Glu Trp Pro Trp Gln Ala Ser Val Arg Arg Gln Gly Ala His Ile Cys
 65   70   75   80

Ser Gly Ser Leu Val Ala Asp Thr Trp Val Leu Thr Ala Ala His Cys
                85   90   95

Phe Glu Lys Ala Ala Ala Thr Glu Leu Asn Ser Trp Ser Val Val Leu
            100   105   110

Gly Ser Leu Gln Arg Glu Gly Leu Ser Pro Gly Ala Glu Glu Val Gly
            115   120   125

Val Ala Ala Leu Gln Leu Pro Arg Ala Tyr Asn His Tyr Ser Gln Gly
        130   135   140

Ser Asp Leu Ala Leu Leu Gln Leu Ala His Pro Thr Thr His Thr Pro
145   150   155   160

Leu Cys Leu Pro Gln Pro Ala His Arg Phe Pro Phe Gly Ala Ser Cys
                165   170   175

Trp Ala Thr Gly Trp Asp Gln Asp Thr Ser Asp Ala Pro Gly Thr Leu

```
                 180                    185                    190

Arg Asn Leu Arg Leu Arg Leu Ile Ser Arg Pro Thr Cys Asn Cys Ile
        195             200             205

Tyr Asn Gln Leu His Gln Arg His Leu Ser Asn Pro Ala Arg Pro Gly
    210             215             220

Met Leu Cys Gly Gly Pro Gln Pro Gly Val Gln Gly Pro Cys Gln Gly
225             230             235             240

Asp Ser Gly Gly Pro Val Leu Cys Leu Glu Pro Asp Gly His Trp Val
            245             250             255

Gln Ala Gly Ile Ile Ser Phe Ala Ser Ser Cys Ala Gln Glu Asp Ala
            260             265             270

Pro Val Leu Leu Thr Asn Thr Ala Ala His Ser Ser Trp Leu Gln Ala
            275             280             285

Arg Val Gln Gly Ala Ala Phe Leu Ala Gln Ser Pro Glu Thr Pro Glu
    290             295             300

Met Ser Asp Glu Asp Ser Cys Val Ala Cys Gly Ser Leu Arg Thr Ala
305             310             315             320

Gly Pro Gln Ala Gly Ala Pro Ser Pro Trp Pro Trp Glu Ala Arg Leu
            325             330             335

Met His Gln Gly Gln Leu Ala Cys Gly Gly Ala Leu Val Ser Glu Glu
            340             345             350

Ala Val Leu Thr Ala Ala His Cys Phe Ile Gly Arg Gln Ala Pro Glu
            355             360             365

Glu Trp Ser Val Gly Leu Gly Thr Arg Pro Glu Glu Trp Gly Leu Lys
    370             375             380

Gln Leu Ile Leu His Gly Ala Tyr Thr His Pro Glu Gly Gly Tyr Asp
385             390             395             400

Met Ala Leu Leu Leu Leu Ala Gln Pro Val Thr Leu Gly Ala Ser Leu
            405             410             415

Arg Pro Leu Cys Leu Pro Tyr Pro Asp His His Leu Pro Asp Gly Glu
            420             425             430

Arg Gly Trp Val Leu Gly Arg Ala Arg Pro Gly Ala Gly Ile Ser Ser
            435             440             445

Leu Gln Thr Val Pro Val Thr Leu Leu Gly Pro Arg Ala Cys Ser Arg
    450             455             460

Leu His Ala Ala Pro Gly Gly Asp Gly Ser Pro Ile Leu Pro Gly Met
465             470             475             480

Val Cys Thr Ser Ala Val Gly Glu Leu Pro Ser Cys Glu
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63

<210> 66
<211> 189
<212> PRT
<213> human

<400> 66
Met Ser Asp Glu Asp Ser Cys Val Ala Cys Gly Ser Leu Arg Thr Ala
 1   5   10   15

Gly Pro Gln Ala Gly Ala Pro Ser Pro Trp Pro Trp Glu Ala Arg Leu
             20   25   30

Met His Gln Gly Gln Leu Ala Cys Gly Gly Ala Leu Val Ser Glu Glu
         35   40   45

Ala Val Leu Thr Ala Ala His Cys Phe Ile Gly Arg Gln Ala Pro Glu
     50   55   60

Glu Trp Ser Val Gly Leu Gly Thr Arg Pro Glu Glu Trp Gly Leu Lys
65   70   75   80

Gln Leu Ile Leu His Gly Ala Tyr Thr His Pro Glu Gly Gly Tyr Asp
                 85   90   95

Met Ala Leu Leu Leu Leu Ala Gln Pro Val Thr Leu Gly Ala Ser Leu
             100   105   110

Arg Pro Leu Cys Leu Pro Tyr Ala Asp His His Leu Pro Asp Gly Glu
         115   120   125

Arg Gly Trp Val Leu Gly Arg Ala Arg Pro Gly Ala Gly Ile Ser Ser
     130   135   140

Leu Gln Thr Val Pro Val Thr Leu Leu Gly Pro Arg Ala Cys Ser Arg
145   150   155   160

Leu His Ala Ala Pro Gly Gly Asp Gly Ser Pro Ile Leu Pro Gly Met
             165   170   175

Val Cys Thr Ser Ala Val Gly Glu Leu Pro Ser Cys Glu
             180   185

<210> 67
<211> 186
<212> DNA
<213> human

<400> 67
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ccagcg   186

<210> 68
<211> 180
<212> DNA
<213> human

<400> 68
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<210> 69
<211> 157
<212> DNA
<213> human

<400> 69
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<210> 70
<211> 157
<212> DNA
<213> human

<400> 70
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<210> 71
<211> 842
<212> DNA
<213> human

<400> 71
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gccctattct gccggggatg gtgtgtacca gtgctgtggg tgagctgccc agctgtgagg 840
gc   842

65

<210> 72
<211> 768
<212> DNA
<213> human

<400> 72
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<210> 73
<211> 279
<212> PRT
<213> human

<400> 73
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Arg His Leu Ser Asn Pro Ala Arg Pro Gly Met Leu Cys Gly Gly Pro
 1               5                  10                  15

Gln Pro Gly Val Gln Gly Pro Cys Gln Gly Asp Ser Gly Gly Pro Val
            20                  25                  30

Leu Cys Leu Glu Pro Asp Gly His Trp Val Gln Ala Gly Ile Ile Ser
        35                  40                  45

Phe Ala Ser Ser Cys Ala Gln Glu Asp Ala Pro Val Leu Leu Thr Asn
    50                  55                  60

Thr Ala Ala His Ser Ser Trp Leu Gln Ala Arg Val Gln Gly Ala Ala
65                  70                  75                  80

Phe Leu Ala Gln Ser Pro Glu Thr Pro Glu Met Ser Asp Glu Asp Ser
                85                  90                  95

Cys Val Ala Cys Gly Ser Leu Arg Thr Ala Gly Pro Gln Ala Gly Ala
            100                 105                 110

Pro Ser Pro Trp Pro Trp Glu Ala Arg Leu Met His Gln Gly Gln Leu
            115                 120                 125

Ala Cys Gly Gly Ala Leu Val Ser Glu Glu Ala Val Leu Thr Ala Ala
    130                 135                 140

His Cys Phe Ile Gly Arg Gln Ala Pro Glu Glu Trp Ser Val Gly Leu
145                 150                 155                 160
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Gly Thr Arg Pro Glu Glu Trp Gly Leu Lys Gln Leu Ile Leu His Gly
            165                 170                 175

Ala Tyr Thr His Pro Glu Gly Gly Tyr Asp Met Ala Leu Leu Leu Leu
            180                 185                 190

Ala Gln Pro Val Thr Leu Gly Ala Ser Leu Arg Pro Leu Cys Leu Pro
            195                 200                 205

Tyr Pro Asp His His Leu Pro Asp Gly Glu Arg Gly Trp Val Leu Gly
    210                 215                 220

Arg Ala Arg Pro Gly Ala Gly Ile Ser Ser Leu Gln Thr Val Pro Val
225                 230                 235                 240

Thr Leu Leu Gly Pro Arg Ala Cys Ser Arg Leu His Ala Ala Pro Gly
            245                 250                 255

Gly Asp Gly Ser Pro Ile Leu Pro Gly Met Val Cys Thr Ser Ala Val
            260                 265                 270

Gly Glu Leu Pro Ser Cys Glu
            275
```

<210> 74
<211> 189
<212> PRT
<213> human

<400> 74

```
Met Ser Asp Glu Asp Ser Cys Val Ala Cys Gly Ser Leu Arg Thr Ala
1               5                   10                  15

Gly Pro Gln Ala Gly Ala Pro Ser Pro Trp Pro Trp Glu Ala Arg Leu
            20                  25                  30

Met His Gln Gly Gln Leu Ala Cys Gly Gly Ala Leu Val Ser Glu Glu
            35                  40                  45

Ala Val Leu Thr Ala Ala His Cys Phe Ile Gly Arg Gln Ala Pro Glu
    50                  55                  60

Glu Trp Ser Val Gly Leu Gly Thr Arg Pro Glu Glu Trp Gly Leu Lys
65                  70                  75                  80

Gln Leu Ile Leu His Gly Ala Tyr Thr His Pro Glu Gly Gly Tyr Asp
                85                  90                  95

Met Ala Leu Leu Leu Leu Ala Gln Pro Val Thr Leu Gly Ala Ser Leu
            100                 105                 110

Arg Pro Leu Cys Leu Pro Tyr Ala Asp His His Leu Pro Asp Gly Glu
            115                 120                 125

Arg Gly Trp Val Leu Gly Arg Ala Arg Pro Gly Ala Gly Ile Ser Ser
    130                 135                 140
```

67

```
Leu Gln Thr Val Pro Val Thr Leu Leu Gly Pro Arg Ala Cys Ser Arg
145             150             155             160


Leu His Ala Ala Pro Gly Gly Asp Gly Ser Pro Ile Leu Pro Gly Met
                165             170             175


Val Cys Thr Ser Ala Val Gly Glu Leu Pro Ser Cys Glu
                180             185
```

```
<210> 75
<211> 342
<212> DNA
<213> human

<400> 75
agctggctgc cccggcctgc aggttggatg dacagcagcc ctggccctgt gcccacctac 60
ctgctcctgg gcgggcccgt cccagaaccc agccacgctc cccatcaggc aggtggtggt 120
caggataggg caggcagagg ggccgcaggc tggctcccag tgtcacaggc tgggccagca 180
gcaggagggc catgtcgtag cccccctcag ggtgggtgta ggctccatgc aggatgagct 240
gcttcaggcc ccactcctcc ggtctggtcc ccagccctac gctccattcc tctggggcct 300
ggcgcccaat gaagcagtgg cagcagtta gcaccgcctc ct 342
```

```
<210> 76
<211> 63
<212> DNA
<213> human

<400> 76
ttggtgtgaa aatttctttt tttgggggggc agcagttttc cttttttttaa acttaaataa 60
att 63
```

```
<210> 77
<211> 1359
<212> DNA
<213> human

<400> 77
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agaccgtcgc gcgcgggcag cgcccccgga cgtctgcccc ctcccgcgcc ggtgccctgc 120
tgctgctgct tctgttgctg aggtctgcag gttgctgggg cgcaggggaa gccccggggg 180
cgctgtccac tgctgatccc gccgaccaga gcgtccagtg tgtccccaag gccacctgtc 240
cttccagccg gcctcgcctt ctctggcaga ccccgaccac ccagacactg ccctcgacca 300
ccatggagac ccaattccca gtttctgaag gcaaagtcga cccataccgc tcctgtggct 360
tttcctacga gcaggacccc accctcaggg acccagaagc cgtggctcgg cggtggccct 420
ggatggtcag cgtgcgggcc aatggcacac acatctgtgc cggcaccatc attgcctccc 480
agtgggtgct gactgtggcc cactgcctga tctggcgtga tgttatctac tcagtgaggg 540
tggggagtcc gtggattgac cagatgacgc agaccgcctc cgatgtcccg gtgctccagg 600
tcatcatgca tagcaggtac cgggcccagc ggttctggtc ctgggtgggc caggccaacg 660
acatcggcct cctcaagctc aagcaggaac tcaagtacag caattacgtg cggcccatct 720
gcctgcctgg cacggactat gtgttgaagg accattcccg ctgcactgtg acgggctggg 780
gactttccaa ggctgacggc atgtggcctc agttccggac cattcaggag aaggaagtca 840
tcatcctgaa caacaaagag tgtgacaatt tctaccacaa cttcaccaaa atccccactc 900
tggttcagat catcaagtcc cagatgatgt gtgcggagga cacccacagg gagaagttct 960
```

```
gctatgagct aactggagag cccttggtct gctccatgga gggcacgtgg tacctggtgg 1020
gattggtgag ctggggtgca ggctgccaga agagcgaggc cccacccatc tacctacagg 1080
tctcctccta ccaacactgg atctgggact gcctcaacgg gcaggccctg gccctgccag 1140
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gactctgtgt gccctccctc acttgtgggc cccccttgcc tccgtgccca ggttgctgtg 1260
ggtgcagctg tcacagccct gagagtcagg gtggagatga ggtgctcaat taaacattac 1320
tgttttccat gtaaaaaaaa aaaaaaaaaa aaaaaaaa                          1359
```

<210> 78
<211> 385
<212> PRT
<213> human

<400> 78

```
Met Gly Arg Trp Cys Gln Thr Val Ala Arg Gly Gln Arg Pro Arg Thr
 1               5                   10                  15
                                                          (

Ser Ala Pro Ser Arg Ala Gly Ala Leu Leu Leu Leu Leu Leu Leu Leu
            20                  25                  30

Arg Ser Ala Gly Cys Trp Gly Ala Gly Glu Ala Pro Gly Ala Leu Ser
        35                  40                  45

Thr Ala Asp Pro Ala Asp Gln Ser Val Gln Cys Val Pro Lys Ala Thr
        50                  55                  60

Cys Pro Ser Ser Arg Pro Arg Leu Leu Trp Gln Thr Pro Thr Thr Gln
65                  70                  75                  80

Thr Leu Pro Ser Thr Thr Met Glu Thr Gln Phe Pro Val Ser Glu Gly
                85                  90                  95

Lys Val Asp Pro Tyr Arg Ser Cys Gly Phe Ser Tyr Glu Gln Asp Pro
            100                 105                 110

Thr Leu Arg Asp Pro Glu Ala Val Ala Arg Arg Trp Pro Trp Met Val
            115                 120                 125

Ser Val Arg Ala Asn Gly Thr His Ile Cys Ala Gly Thr Ile Ile Ala
    130                 135                 140

Ser Gln Trp Val Leu Thr Val Ala His Cys Leu Ile Trp Arg Asp Val
145                 150                 155                 160

Ile Tyr Ser Val Arg Val Gly Ser Pro Trp Ile Asp Gln Met Thr Gln
                165                 170                 175

Thr Ala Ser Asp Val Pro Val Leu Gln Val Ile Met His Ser Arg Tyr
            180                 185                 190

Arg Ala Gln Arg Phe Trp Ser Trp Val Gly Gln Ala Asn Asp Ile Gly
        195                 200                 205

Leu Leu Lys Leu Lys Gln Glu Leu Lys Tyr Ser Asn Tyr Val Arg Pro
210                 215                 220
```

69

```
Ile Cys Leu Pro Gly Thr Asp Tyr Val Leu Lys Asp His Ser Arg Cys
225             230         235             240

Thr Val Thr Gly Trp Gly Leu Ser Lys Ala Asp Gly Met Trp Pro Gln
                245             250             255

Phe Arg Thr Ile Gln Glu Lys Glu Val Ile Ile Leu Asn Asn Lys Glu
            260             265             270

Cys Asp Asn Phe Tyr His Asn Phe Thr Lys Ile Pro Thr Leu Val Gln
        275             280             285

Ile Ile Lys Ser Gln Met Met Cys Ala Glu Asp Thr His Arg Glu Lys
    290             295             300

Phe Cys Tyr Glu Leu Thr Gly Glu Pro Leu Val Cys Ser Met Glu Gly
305             310             315             320

Thr Trp Tyr Leu Val Gly Leu Val Ser Trp Gly Ala Gly Cys Gln Lys
            325             330             335

Ser Glu Ala Pro Pro Ile Tyr Leu Gln Val Ser Ser Tyr Gln His Trp
            340             345             350

Ile Trp Asp Cys Leu Asn Gly Gln Ala Leu Ala Leu Pro Ala Pro Ser
            355             360             365

Arg Thr Leu Leu Leu Ala Leu Pro Leu Pro Leu Ser Leu Leu Ala Ala
    370             375             380

Leu
385


<210> 79
<211> 1943
<212> DNA
<213> human

<400> 79
ggagaagaag ccgagctgag cggatcctca cacgactgtg atccgattct ttccagcggc 60
ttctgcaacc aagcgggtct taccccccggt cctccgcgtc tccagtcctc gcacctggaa 120
ccccaacgtc cccgagagtc cccgaatccc cgctcccagg ctacctaaga ggatgagcgg 180
tgctccgacg gccggggcag ccctgatgct ctgcgccgcc accgccgtgc tactgagcgc 240
tcagggcgga cccgtgcagt ccaagtcgcc gcgctttgcg tcctgggacg agatgaatgt 300
cctggcgcac ggactcctgc agctcggcca ggggctgcgc gaacacgcgg agcgcacccg 360
cagtcagctg agcgcgctgg agcggcgcct gagcgcgtgc gggtccgcct gtcagggaac 420
cgaggggtcc accgacctcc cgttagcccc tgagagccgg gtggaccctg aggtccttca 480
cagcctgcag acacaactca aggctcagaa cagcaggatc cagcaactct tccacaaggt 540
ggcccagcag cagcggcacc tggagaagca gcacctgcga attcagcatc tgcaaagcca 600
gtttggcctc ctggaccaca agcacctaga ccatgaggtg gccaagcctg cccgaagaaa 660
gaggctgccc gagatggccc agccagttga cccggctcac aatgtcagcc gcctgcaccg 720
gctgcccagg gattgccagg agctgttcca ggttggggag aggcagagtg gactatttga 780
aatccagcct caggggtctc cgccattttt ggtgaactgc aagatgacct cagatggagg 840
ctggacagta attcagaggc gccacgatgg ctcagtggac ttcaaccggc cctgggaagc 900
ctacaaggcg gggtttgggg atccccacgg cgagttctgg ctgggtctgg agaaggtgca 960
tagcatcacg ggggaccgca acagccgcct ggccgtgcag ctgcgggact gggatggcaa 1020
```

70

```
cgccgagttg ctgcagttct ccgtgcacct gggtggcgag gacacggcct atagcctgca 1080
gctcactgca cccgtggccg gccagctggg cgccaccacc gtcccaccca gcggcctctc 1140
cgtacccttc tccacttggg accaggatca cgacctccgc agggacaaga actgcgccaa 1200
gagcctctct ggaggctggt ggtttggcac ctgcagccat tccaacctca acggccagta 1260
cttccgctcc atcccacagc agcggcagaa gcttaagaag ggaatcttct ggaagacctg 1320
gcggggccgc tactacccgc tgcaggccac caccatgttg atccagccca tggcagcaga 1380
ggcagcctcc tagcgtcctg gctgggcctg gtcccaggcc cacgaaagac ggtgactctt 1440
ggctctgccc gaggatgtgg ccgttccctg cctgggcagg ggctccaagg aggggccatc 1500
tggaaacttg tggacagaga agaagaccac gactggagaa gccccctttc tgagtgcagg 1560
ggggctgcat gcgttgcctc ctgagatcga ggctgcagga tatgctcaga ctctagaggc 1620
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accacttggg gccagccaga ctggcctcaa tggcggactc agtcacattg actgacgggg 1740
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cctggggaca caagcaggcg ccaatggtat ctgggcggcg tcacagagtt cttggaataa 1860
aagcaacctc agaacactta aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1920
aaaaaaaaaa aaaaaaaaaa aaa                                        1943
```

<210> 80
<211> 406
<212> PRT
<213> human

<400> 80

```
Met Ser Gly Ala Pro Thr Ala Gly Ala Ala Leu Met Leu Cys Ala Ala
  1               5                  10                  15

Thr Ala Val Leu Leu Ser Ala Gln Gly Gly Pro Val Gln Ser Lys Ser
             20                  25                  30

Pro Arg Phe Ala Ser Trp Asp Glu Met Asn Val Leu Ala His Gly Leu
         35                  40                  45

Leu Gln Leu Gly Gln Gly Leu Arg Glu His Ala Glu Arg Thr Arg Ser
     50                  55                  60

Gln Leu Ser Ala Leu Glu Arg Arg Leu Ser Ala Cys Gly Ser Ala Cys
 65                  70                  75                  80

Gln Gly Thr Glu Gly Ser Thr Asp Leu Pro Leu Ala Pro Glu Ser Arg
                 85                  90                  95

Val Asp Pro Glu Val Leu His Ser Leu Gln Thr Gln Leu Lys Ala Gln
             100                 105                 110

Asn Ser Arg Ile Gln Gln Leu Phe His Lys Val Ala Gln Gln Gln Arg
         115                 120                 125

His Leu Glu Lys Gln His Leu Arg Ile Gln His Leu Gln Ser Gln Phe
     130                 135                 140

Gly Leu Leu Asp His Lys His Leu Asp His Glu Val Ala Lys Pro Ala
145                 150                 155                 160

Arg Arg Lys Arg Leu Pro Glu Met Ala Gln Pro Val Asp Pro Ala His
                 165                 170                 175
```

71

```
Asn Val Ser Arg Leu His Arg Leu Pro Arg Asp Cys Gln Glu Leu Phe
        180                 185                 190

Gln Val Gly Glu Arg Gln Ser Gly Leu Phe Glu Ile Gln Pro Gln Gly
        195                 200                 205

Ser Pro Pro Phe Leu Val Asn Cys Lys Met Thr Ser Asp Gly Gly Trp
    210                 215                 220

Thr Val Ile Gln Arg Arg His Asp Gly Ser Val Asp Phe Asn Arg Pro
225                 230                 235                 240

Trp Glu Ala Tyr Lys Ala Gly Phe Gly Asp Pro His Gly Glu Phe Trp
            245                 250                 255

Leu Gly Leu Glu Lys Val His Ser Ile Thr Gly Asp Arg Asn Ser Arg
        260                 265                 270

Leu Ala Val Gln Leu Arg Asp Trp Asp Gly Asn Ala Glu Leu Leu Gln
        275                 280                 285

Phe Ser Val His Leu Gly Gly Glu Asp Thr Ala Tyr Ser Leu Gln Leu
    290                 295                 300

Thr Ala Pro Val Ala Gly Gln Leu Gly Ala Thr Thr Val Pro Pro Ser
305                 310                 315                 320

Gly Leu Ser Val Pro Phe Ser Thr Trp Asp Gln Asp His Asp Leu Arg
            325                 330                 335

Arg Asp Lys Asn Cys Ala Lys Ser Leu Ser Gly Gly Trp Trp Phe Gly
        340                 345                 350

Thr Cys Ser His Ser Asn Leu Asn Gly Gln Tyr Phe Arg Ser Ile Pro
        355                 360                 365

Gln Gln Arg Gln Lys Leu Lys Lys Gly Ile Phe Trp Lys Thr Trp Arg
        370                 375                 380

Gly Arg Tyr Tyr Pro Leu Gln Ala Thr Thr Met Leu Ile Gln Pro Met
385                 390                 395                 400

Ala Ala Glu Ala Ala Ser
            405
```

```
<210> 81
<211> 731
<212> DNA
<213> human

<400> 81
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tcaactggct gggccatctc gggcagcctc tttcttcggg caggcttggc cacctcatgg 120
tctaggtgct tgtggtccag gaggccaaac tggctttgca gatgctgaat cgcaggtgc 180
tgcttctcca ggtgccgctg ctgctgggcc accttgtgga agagttgctg gatcctgctg 240
ttctgagcct tgagttgtgt ctgcaggctg tgaaggacct cagggtccac ccggctctca 300
```

72

```
ggggctaacg ggaggtcggt ggacccctcg gttccctgac aggcggaccc gcacgcgctc 360
aggcgccgct ccagcgcgct cagctgactg cgggtgcgct ccgcgtgttc gcgcagcccc 420
tggccgagct gcaggagtcc gtgcgccagg acattcatct cgtcccagga cgcaaagcgc 480
ggcgacttgg actgcacggg tccgccctga gcgctcagta gcacggcggt ggcggcgcag 540
agcatcaggg ctgccccggc cgtcggagca ccgctcatcc tcttaggtag cctgggagcg 600
gggattcggg gactctcggg gacgttgggg ttccaggtgc gaggactgga gacgcggagg 660
accggggggta agacccgctt ggttgcagaa gccgctggaa agaatcggat cacagtcgtg 720
tgaggatccg c                                                       731
```

<210> 82
<211> 730
<212> DNA
<213> human

<400> 82
```
tggaacagct cctggcaatc cctgggcagc cggtgcaggc ggctgacatt gtgagccggg 60
tcaactggct gggccatctc gggcagcctc tttcttcggg caggcttggc cacctcatgg 120
tctaggtgct tgtggtccag gaggccaaac tggctttgca gatgctgaat cgcaggtgc 180
tgcttctcca ggtgccgctg ctgctgggcc accttgtgga agagttgctg gatcctgctg 240
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ggggctaacg ggaggtcggt ggaccccctcg gttccctgac aggcggaccc gcacgcgctc 360
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ggccgagctg caggagtccg tgcgccagga cattcatctc gtcccaggac gcaaagcgcg 480
gcgacttgga ctgcacgggt ccgccctgag cgctcagtag cacggcggtg gcggcgcaga 540
gcatcaggggc tgccccggcc gtcggagcac cgctcatcct cttaggtagc ctgggagcgg 600
ggattcgggg actctcgggg acgttggggt tccaggtgcg aggactggag acgcggagga 660
ccggggggtaa gacccgcttg gttgcagaag ccgctggaaa gaatcggatc acagtcgtgt 720
gaggatccgc                                                         730
```

<210> 83
<211> 403
<212> DNA
<213> human

<400> 83
```
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agatgctgaa ttcgcaggtg ctgcttctcc aggtgccgct gctgctgggc caccttgtgg 120
aagagttgct ggatcctgct gttctgagcc ttgagttgtg tctgcaggct gtgaaggacc 180
tcaggggtcca cccggctctc aggggctaac gggaggtcgg tggacccctc ggttccctga 240
caggcggacc cgcacgcgct caggcgccgt ttcagcgcgc tcagctgact gcgggtgcgc 300
tccgcgtgtt cgcgcagccc ctggccgagc tgcaggagtc cgtgcgccag gacattcatc 360
tcgtcccagg acgcaaagcg cggcgacttg gactgcacgg gtc                     403
```

<210> 84
<211> 245
<212> DNA
<213> human

<400> 84
```
cagagccaag agtcaccgtc tttcgtgggc ctgggaccag gcccagccag gacgctagga 60
ggctgcctct gctgccatgg gctggatcaa catggtggtg gcctgcagcg ggtagtagcg 120
gccccgccag gtcttccaga agattcccttcttaagcttc tgccgctgct gtgggatgga 180
gcggaagtac tggccgttga ggttggaatg gctgcaggtg ccaaaccacc agcctccaga 240
gaggc                                                              245
```

<210> 85
<211> 245
<212> DNA
<213> human

<400> 85
cagagccaag agtcaccgtc tttcgtgggc ctgggaccag gcccagccag gacgctagga 60
ggctgcctct gctgccatgg gctggatcaa catggtggtg gcctgcagcg ggtagtagcg 120
gccccgccag gtcttccaga agattccctt cttaagcttc tgccgctgct gtgggatgga 180
gcggaagtac tggccgttga ggttggaatg gctgcaggtg ccaaaccacc agcctccaga 240
gaggc   245

<210> 86
<211> 159
<212> DNA
<213> human

<400> 86
aagcttaaga agggaatctt ctggaagacc tggcggggcc gctactaccc gctgcaggcc 60
accaccatgt tgatccagcc catggcagca gaggcagcct cctagcgtcc tggctgggcc 120
tggtcccagg ccaacgaaag acggtgactc ttggctccg   159

<210> 87
<211> 1943
<212> DNA
<213> human

<400> 87
ggagaagaag ccgagctgag cggatcctca cacgactgtg atccgattct ttccagcggc 60
ttctgcaacc aagcgggtct tacccccggt cctccgcgtc tccagtcctc gcacctggaa 120
ccccaacgtc cccgagagtc cccgaatccc cgctcccagg ctacctaaga ggatgagcgg 180
tgctccgacg gccggggcag ccctgatgct ctgcgccgcc accgccgtgc tactgagcgc 240
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cctggcgcac ggactcctgc agctcggcca ggggctgcgc gaacacgcgg agcgcacccg 360
cagtcagctg agcgcgctgg agcggcgcct gagcgcgtgc gggtccgcct gtcagggaac 420
cgaggggtcc accgacctcc cgttagcccc tgagagccgg gtggaccctg aggtccttca 480
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ggcccagcag cagcggcacc tggagaagca gcacctgcga attcagcatc tgcaaagcca 600
gtttggcctc ctggaccaca agcacctaga ccatgaggtg gccaagcctg cccgaagaaa 660
gaggctgccc gagatggccc agccagttga cccggctcac aatgtcagcc gcctgcaccg 720
gctgcccagg gattgccagg agctgttcca ggttggggag aggcagagtg gactatttga 780
aatccagcct caggggtctc cgccattttt ggtgaactgc aagatgacct cagatggagg 840
ctggacagta attcagaggc gccacgatgg ctcagtggac ttcaaccggc cctgggaagc 900
ctacaaggcg gggtttgggg atccccacgg cgagttctgg ctgggtctgg agaaggtgca 960
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gctcactgca cccgtggccg gccagctggg cgccaccacc gtcccaccca gcggcctctc 1140
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gagcctctct ggaggctggt ggtttggcac ctgcagccat tccaacctca acggccagta 1260
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gcggggccgc tactacccgc tgcaggccac caccatgttg atccagccca tggcagcaga 1380
ggcagcctcc tagcgtcctg gctgggcctg gtcccaggcc cacgaaagac ggtgactctt 1440
ggctctgccc gaggatgtgg ccgttccctg cctgggcagg ggctccaagg agggccatc 1500

```
tggaaacttg tggacagaga agaagaccac gactggagaa gccccctttc tgagtgcagg 1560
ggggctgcat gcgttgcctc ctgagatcga ggctgcagga tatgctcaga ctctagaggc 1620
gtggaccaag gggcatggag cttcactcct tgctggccag ggagttgggg actcagaggc 1680
accacttggg gccagccaga ctggcctcaa tggcggactc agtcacattg actgacgggg 1740
accagggctt gtgtgggtcg agagcgccct catggtgctg gtgctgttgt gtgtaggtcc 1800
cctggggaca caagcaggcg ccaatggtat ctgggcggcg tcacagagtt cttggaataa 1860
aagcaacctc agaacactta aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1920
aaaaaaaaaa aaaaaaaaaa aaa                                         1943
```

<210> 88
<211> 406
<212> PRT
<213> human

<400> 88

```
Met Ser Gly Ala Pro Thr Ala Gly Ala Ala Leu Met Leu Cys Ala Ala
  1               5                  10                  15

Thr Ala Val Leu Leu Ser Ala Gln Gly Gly Pro Val Gln Ser Lys Ser
             20                  25                  30

Pro Arg Phe Ala Ser Trp Asp Glu Met Asn Val Leu Ala His Gly Leu
         35                  40                  45

Leu Gln Leu Gly Gln Gly Leu Arg Glu His Ala Glu Arg Thr Arg Ser
     50                  55                  60

Gln Leu Ser Ala Leu Glu Arg Arg Leu Ser Ala Cys Gly Ser Ala Cys
 65                  70                  75                  80

Gln Gly Thr Glu Gly Ser Thr Asp Leu Pro Leu Ala Pro Glu Ser Arg
                 85                  90                  95

Val Asp Pro Glu Val Leu His Ser Leu Gln Thr Gln Leu Lys Ala Gln
            100                 105                 110

Asn Ser Arg Ile Gln Gln Leu Phe His Lys Val Ala Gln Gln Gln Arg
            115                 120                 125

His Leu Glu Lys Gln His Leu Arg Ile Gln His Leu Gln Ser Gln Phe
    130                 135                 140

Gly Leu Leu Asp His Lys His Leu Asp His Glu Val Ala Lys Pro Ala
145                 150                 155                 160

Arg Arg Lys Arg Leu Pro Glu Met Ala Gln Pro Val Asp Pro Ala His
                165                 170                 175

Asn Val Ser Arg Leu His Arg Leu Pro Arg Asp Cys Gln Glu Leu Phe
            180                 185                 190

Gln Val Gly Glu Arg Gln Ser Gly Leu Phe Glu Ile Gln Pro Gln Gly
            195                 200                 205

Ser Pro Pro Phe Leu Val Asn Cys Lys Met Thr Ser Asp Gly Gly Trp
    210                 215                 220
```

```
Thr Val Ile Gln Arg Arg His Asp Gly Ser Val Asp Phe Asn Arg Pro
225             230             235             240

Trp Glu Ala Tyr Lys Ala Gly Phe Gly Asp Pro His Gly Glu Phe Trp
                245             250             255

Leu Gly Leu Glu Lys Val His Ser Ile Thr Gly Asp Arg Asn Ser Arg
                260             265             270

Leu Ala Val Gln Leu Arg Asp Trp Asp Gly Asn Ala Glu Leu Leu Gln
                275             280             285

Phe Ser Val His Leu Gly Gly Glu Asp Thr Ala Tyr Ser Leu Gln Leu
    290             295             300

Thr Ala Pro Val Ala Gly Gln Leu Gly Ala Thr Thr Val Pro Pro Ser
305             310             315             320

Gly Leu Ser Val Pro Phe Ser Thr Trp Asp Gln Asp His Asp Leu Arg
                325             330             335

Arg Asp Lys Asn Cys Ala Lys Ser Leu Ser Gly Gly Trp Trp Phe Gly
                340             345             350

Thr Cys Ser His Ser Asn Leu Asn Gly Gln Tyr Phe Arg Ser Ile Pro
                355             360             365

Gln Gln Arg Gln Lys Leu Lys Lys Gly Ile Phe Trp Lys Thr Trp Arg
                370             375             380

Gly Arg Tyr Tyr Pro Leu Gln Ala Thr Thr Met Leu Ile Gln Pro Met
385             390             395             400

Ala Ala Glu Ala Ala Ser
                405
```

<210> 89
<211> 527
<212> DNA
<213> human

<400> 89
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cagagccaag agtcaccgtc tttcgtgggc ctgggaccag gcccagccag gacgctagga 60
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gccccgccag gtcttccaga agattccctt cttaagcttc tgccgctgct gtgggatgga 180
gcggaagtac tggccgttga ggttggaatg gctgcaggtg ccaaaccacc agcctccaga 240
gaggctcttg gcgcagttct tgtccctgcg gaggtcgtga tcctggtccc aagtggagaa 300
gggtacggag aggccgctgg gtgggacggt ggtggcgccc agctggccgg ccacgggtgc 360
agtgagctgc aggctatagg ccgtgtcctc gccacccagg tgcacggaga actgcagcaa 420
ctcggcgttg ccatcccagt cccgcagctg cacggccagg cggctgttgc ggtcccccat 480
gatgctatgc accttctcca gacccagcca gaactcgccg tggggat      527
```

<210> 90
<211> 547

<212> DNA
<213> human

<400> 90

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cagagccaag agtcaccgtc tttcgtgggc ctgggaccag gcccagccag gacgctagga 60
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gccccgccag gtcttccaga agattccctt cttaagcttc tgccgctgct gtgggatgga 180
gcggaagtac tggccgttga ggttggaatg gctgcaggtg ccaaaccacc agcctccaga 240
gaggctcttg gcgcagttct tgtccctgcg gaggtcgtga tcctggtccc aagtggagaa 300
gggtacggag aggccgctgg gtgggacggt ggtggcgccc agctggccgg ccacgggtgc 360
agtgagctgc aggctatagg ccgtgtcctc gccacccagg tgcacggaga actgcagcaa 420
ctcggcgttg ccatcccagt cccgcagctg cacggccagg cggctgttgc ggtcccccgt 480
gatgctatgc accttctcca gacccagcca gaactcgcct ggagtgggag aggccactcc 540
atgaggc                                                         547
```

<210> 91
<211> 399
<212> DNA
<213> human

<400> 91

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gttgctggat cctgctgttc tgagccttga gttgtgtctg caggctgtga aggacctcag 180
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cggacccgca cgcgctcagg cgccgtttca gcgcgctcag ctgactgcgg gtgcgctccg 300
cgtgttcgcg cagcccctgg ccgagctgca ggagtccgtg cgccaggaca ttcatctcgt 360
cccaggacgc aaagcgcggc gacttggact gcacgggtc                       399
```

<210> 92
<211> 204
<212> DNA
<213> human

<400> 92

```
ggtgcaggcg gctgacattg tgagccgggt caactggctg ggccatctcg ggcagcctct 60
ttcttcgggc aggcttggcc acctcatggt ctaggtgctt gtggtccagg aggccaaact 120
ggctttgcag atgctgaatt cgcaggtgct gcttctccag gtgccgctgc tgctgggcca 180
ccttgtggaa gagttgctgg atcc                                       204
```

<210> 93
<211> 204
<212> DNA
<213> human

<400> 93

```
ggtgcaggcg gctgacattg tgagccgggt caactggctg ggccatctcg ggcagcctct 60
ttcttcgggc aggcttggcc acctcatggt ctaggtgctt gtggtccagg aggccaaact 120
ggctttgcag atgctgaatt cgcaggtgct gcttctccag gtgccgctgc tgctgggcca 180
ccttgtggaa gagttgctgg atcc                                       204
```

<210> 94
<211> 1943

77

<212> DNA
<213> human

<400> 94
```
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ttctgcaacc aagcgggtct taccccceggt cctccgcgtc tccagtcctc gcacctggaa 120
ccccaacgtc cccgagagtc cccgaatccc cgctcccagg ctacctaaga ggatgagcgg 180
tgctccgacg gccggggcag ccctgatgct ctgcgccgcc accgccgtgc tactgagcgc 240
tcagggcgga cccgtgcagt ccaagtcgcc gcgctttgcg tcctgggacg agatgaatgt 300
cctggcgcac ggactcctgc agctcggcca ggggctgcgc gaacacgcgg agcgcacccg 360
cagtcagctg agcgcgctgg agcggcgcct gagcgcgtgc gggtccgcct gtcagggaac 420
cgaggggtcc accgacctcc cgttagcccc tgagagccgg gtggaccctg aggtccttca 480
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gtttggcctc ctggaccaca agcacctaga ccatgaggtg gccaagcctg cccgaagaaa 660
gaggctgccc gagatggccc agccagttga cccggctcac aatgtcagcc gcctgcaccg 720
gctgcccagg gattgccagg agctgttcca ggttggggag aggcagagtg gactatttga 780
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cctggggaca caagcaggcg ccaatggtat ctgggcggcg tcacagagtt cttggaataa 1860
aagcaacctc agaacactta aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1920
aaaaaaaaaa aaaaaaaaaa aaa                                         1943
```

<210> 95
<211> 406
<212> PRT
<213> human

<400> 95
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Met Ser Gly Ala Pro Thr Ala Gly Ala Ala Leu Met Leu Cys Ala Ala
1               5                   10                  15

Thr Ala Val Leu Leu Ser Ala Gln Gly Gly Pro Val Gln Ser Lys Ser
            20                  25                  30

Pro Arg Phe Ala Ser Trp Asp Glu Met Asn Val Leu Ala His Gly Leu
        35                  40                  45

Leu Gln Leu Gly Gln Gly Leu Arg Glu His Ala Glu Arg Thr Arg Ser
    50                  55                  60
```

```
Gln Leu Ser Ala Leu Glu Arg Arg Leu Ser Ala Cys Gly Ser Ala Cys
65              70              75                          80

Gln Gly Thr Glu Gly Ser Thr Asp Leu Pro Leu Ala Pro Glu Ser Arg
                85              90                  95

Val Asp Pro Glu Val Leu His Ser Leu Gln Thr Gln Leu Lys Ala Gln
            100             105             110

Asn Ser Arg Ile Gln Gln Leu Phe His Lys Val Ala Gln Gln Gln Arg
            115             120             125

His Leu Glu Lys Gln His Leu Arg Ile Gln His Leu Gln Ser Gln Phe
    130             135             140

Gly Leu Leu Asp His Lys His Leu Asp His Glu Val Ala Lys Pro Ala
145             150             155             160

Arg Arg Lys Arg Leu Pro Glu Met Ala Gln Pro Val Asp Pro Pro His
            165             170                 175

Asn Val Ser Arg Leu His Arg Leu Pro Arg Asp Cys Gln Glu Leu Phe
            180             185             190

Gln Val Gly Glu Arg Gln Ser Gly Leu Phe Glu Ile Gln Pro Gln Gly
    195             200             205

Ser Pro Pro Phe Leu Val Asn Cys Lys Met Thr Ser Asp Gly Gly Trp
    210             215             220

Thr Val Ile Gln Arg Arg His Asp Gly Ser Val Asp Phe Asn Arg Pro
225             230             235             240

Trp Glu Ala Tyr Lys Ala Gly Phe Gly Asp Pro His Gly Glu Phe Trp
            245             250             255

Leu Gly Leu Glu Lys Val His Ser Ile Met Gly Asp Arg Asn Ser Arg
            260             265             270

Leu Ala Val Gln Leu Arg Asp Trp Asp Gly Asn Ala Glu Leu Leu Gln
            275             280             285

Phe Ser Val His Leu Gly Gly Glu Asp Thr Ala Tyr Ser Leu Gln Phe
    290             295             300

Thr Ala Pro Val Ala Gly Gln Leu Gly Ala Thr Thr Val Pro Pro Ser
305             310             315             320

Gly Leu Ser Val Pro Phe Ser Thr Trp Asp Gln Asp His Asp Leu Arg
            325             330             335

Arg Asp Lys Asn Cys Ala Lys Ser Leu Ser Gly Gly Trp Trp Phe Gly
            340             345             350

Thr Cys Ser His Ser Asn Leu Asn Gly Gln Tyr Phe Arg Ser Ile Pro
    355             360             365
```

79

```
Gln Gln Arg Gln Lys Leu Lys Lys Gly Ile Phe Trp Lys Thr Trp Arg
    370               375               380

Gly Arg Tyr Tyr Ser Leu Gln Ala Thr Thr Met Leu Ile Gln Pro Met
385               390               395               400

Ala Ala Glu Ala Ala Ser
              405
```

```
<210> 96
<211> 700
<212> DNA
<213> human

<400> 96
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ggctttgcag atgctgaatt cgcaggtgct gcttctccag gtgccgctgc tgctgggcca 180
ccttgtggaa gagttgctgg atcctgctgt tctgagcctt gagttgtgtc tgcaggctgt 240
gaaggacctc agggtccacc cggctctcag gggctaacgg gaggtcggtg gaccccctcgg 300
ttccctgaca ggcggacccg cacgcgctca ggcgccgctc cagcgcgctc agctgactgc 360
gggtgcgctc cgcgtgttcg cgcagcccct ggccgagctg caggagtccg tgcgccagga 420
cattcatctc gtcccaggac gcaaagcgcg gcgacttgga ctgcacgggt ccgccctgag 480
cgctcagtag cacggcggtg gcggcgcaga gcatcagggc tgccccggcc gtcggagcac 540
cgctcatcct cttaggtagc ctgggagcgg ggattcgggg actctcgggg acgttggggt 600
tccaggtgcg aggactggag acgcggagga ccggggtaa gacccgcttg gttgcagaag 660
ccgctggaaa gaatcggatc acagtcgtgt gaggatccgc                       700
```

```
<210> 97
<211> 1943
<212> DNA
<213> human

<400> 97
ggagaagaag ccgagctgag cggatcctca cacgactgtg atccgattct ttccagcggc  60
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ccccaacgtc cccgagagtc cccgaatccc cgctcccagg ctacctaaga ggatgagcgg 180
tgctccgacg gccggggcag ccctgatgct ctgcgccgcc accgccgtgc tactgagcgc 240
tcagggcgga cccgtgcagt ccaagtcgcc gcgctttgcg tcctgggacg agatgaatgt 300
cctggcgcac ggactcctgc agctcggcca ggggctgcgc gaacacgcgg agcgcacccg 360
cagtcagctg agcgcgctgg agcggcgcct gagcgcgtgc gggtccgcct gtcagggaac 420
cgaggggtcc accgacctcc cgttagcccc tgagagccgg gtggaccctg aggtccttca 480
cagcctgcag acacaactca aggctcagaa cagcaggatc cagcaactct ccacaaggt 540
ggcccagcag cagcggcacc tggagaagca gcacctgcga attcagcatc tgcaaagcca 600
gtttggcctc ctggaccaca agcacctaga ccatgaggtg gccaagcctg cccgaagaaa 660
gaggctgccc gagatggccc agccagttga cccggctcac aatgtcagcc gcctgcaccg 720
gctgcccagg gattgccagg agctgttcca ggttggggag aggcagagtg gactatttga 780
aatccagcct caggggtctc cgccattttt ggtgaactgc aagatgacct cagatggagg 840
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ctacaaggcg gggtttgggg atccccacgg cgagttctgg ctgggtctgg agaaggtgca 960
tagcatcacg ggggaccgca acagccgcct ggccgtgcag ctgcgggact gggatggcaa 1020
cgccgagttg ctgcagttct ccgtgcacct gggtggcgag gacacggcct atagcctgca 1080
gctcactgca cccgtggccg gccagctggg cgccaccacc gtcccaccca gcggcctctc 1140
cgtacccttc tccacttggg accaggatca cgacctccgc agggacaaga actgcgccaa 1200
gagcctctct ggaggctggt ggtttggcac ctgcagccat tccaacctca cggccagta 1260
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```
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tggaaacttg tggacagaga agaagaccac gactggagaa gcccccttttc tgagtgcagg 1560
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accacttggg gccagccaga ctggcctcaa tggcggactc agtcacattg actgacgggg 1740
accagggctt gtgtgggtcg agagcgccct catggtgctg gtgctgttgt gtgtaggtcc 1800
cctggggaca caagcaggcg ccaatggtat ctgggcggcg tcacagagtt cttggaataa 1860
aagcaacctc agaacactta aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1920
aaaaaaaaaa aaaaaaaaaa aaa                                       1943
```

<210> 98
<211> 406
<212> PRT
<213> human

<400> 98

```
Met Ser Gly Ala Pro Thr Ala Gly Ala Ala Leu Met Leu Cys Ala Ala
 1               5                  10                  15

Thr Ala Val Leu Leu Ser Ala Gln Gly Gly Pro Val Gln Ser Lys Ser
            20                  25                  30

Pro Arg Phe Ala Ser Trp Asp Glu Met Asn Val Leu Ala His Gly Leu
        35                  40                  45

Leu Gln Leu Gly Gln Gly Leu Arg Glu His Ala Glu Arg Thr Arg Ser
    50                  55                  60

Gln Leu Ser Ala Leu Glu Arg Arg Leu Ser Ala Cys Gly Ser Ala Cys
65                  70                  75                  80

Gln Gly Thr Glu Gly Ser Thr Asp Leu Pro Leu Ala Pro Glu Ser Arg
                85                  90                  95

Val Asp Pro Glu Val Leu His Ser Leu Gln Thr Gln Leu Lys Ala Gln
            100                 105                 110

Asn Ser Arg Ile Gln Gln Leu Phe His Lys Val Ala Gln Gln Gln Arg
        115                 120                 125

His Leu Glu Lys Gln His Leu Arg Ile Gln His Leu Gln Ser Gln Phe
    130                 135                 140

Gly Leu Leu Asp His Lys His Leu Asp His Glu Val Ala Lys Pro Ala
145                 150                 155                 160

Arg Arg Lys Arg Leu Pro Glu Met Ala Gln Pro Val Asp Pro Ala His
                165                 170                 175

Asn Val Ser Arg Leu His Arg Leu Pro Arg Asp Cys Gln Glu Leu Phe
            180                 185                 190

Gln Val Gly Glu Arg Gln Ser Gly Leu Phe Glu Ile Gln Pro Gln Gly
```

81

```
                195                    200                    205

Ser Pro Pro Phe Leu Val Asn Cys Lys Met Thr Ser Asp Gly Gly Trp
    210                 215                 220

Thr Val Ile Gln Arg Arg His Asp Gly Ser Val Asp Phe Asn Arg Pro
225                     230                 235                 240

Trp Glu Ala Tyr Lys Ala Gly Phe Gly Asp Pro His Gly Glu Phe Trp
                245                 250                 255

Leu Gly Leu Glu Lys Val His Ser Ile Thr Gly Asp Arg Asn Ser Arg
                260                 265                 270

Leu Ala Val Gln Leu Arg Asp Trp Asp Gly Asn Ala Glu Leu Leu Gln
                275                 280                 285

Phe Ser Val His Leu Gly Gly Glu Asp Thr Ala Tyr Ser Leu Gln Leu
    290                 295                 300

Thr Ala Pro Val Ala Gly Gln Leu Gly Ala Thr Thr Val Pro Pro Ser
305                 310                 315                 320

Gly Leu Ser Val Pro Phe Ser Thr Trp Asp Gln Asp His Asp Leu Arg
                325                 330                 335

Arg Asp Lys Asn Cys Ala Lys Ser Leu Ser Gly Gly Trp Trp Phe Gly
            340                 345                 350

Thr Cys Ser His Ser Asn Leu Asn Gly Gln Tyr Phe Arg Ser Ile Pro
        355                 360                 365

Gln Gln Arg Gln Lys Leu Lys Lys Gly Ile Phe Trp Lys Thr Trp Arg
    370                 375                 380

Gly Arg Tyr Tyr Pro Leu Gln Ala Thr Thr Met Leu Ile Gln Pro Met
385                 390                 395                 400

Ala Ala Glu Ala Ala Ser
                405
```

```
<400> 99
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acaatgtcag ccgcctgcac catggaggct ggacagtaat tcagaggcgc acgatggct 180
cagtggactt caaccggccc tgggaagcct acaaggcggg gtttggggat ccccacggcg 240
agttctggct gggtctggag aaggtgcata gcatcacggg ggaccgcaac agccgcctgg 300
ccgtgcagct gcgggactgg gatggcaacg ccgagttgct gcagttctcc gtgcacctgg 360
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ccaccaccgt cccacccagc ggcctctccg tacccttctc cacttgggac caggatcacg 480
acctccgcag ggacaagaac tgcgccaaga gcctctctgg aggctggtgg tttggcacct 540
```

82

```
gcagccattc                                                      550
```

<210> 100
<211> 523
<212> DNA
<213> human

<400> 100
```
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aagagttgct ggatcctgct gttctgagcc ttgagttgtg tctgcaggct gtgaaggacc 180
tcagggtcca cccggctctc aggggctaac gggaggtcgg tggacccctc ggttccctga 240
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tccgcgtgtt cgcgcagccc ctggccgagc tgcaggagtc cgtgcgccag gacattcatc 360
tcgtcccagg acgcaaagcg cggcgacttg gactgcacgg gtccgccctg agcgctcagt 420
agcacggcgg tggcggcgca gagcatcagg gctgccccgg ccgtcggagc accgctcatc 480
ctcttaggta gcctgggagc ggggattcgg ggactcttcg ggg                 523
```

<210> 101
<211> 96
<212> DNA
<213> human

<400> 101
```
ggtgcaggcg gctgacattg tgagccgggt caactggctg ggccatctcg ggcagcctct 60
ttcttcgggc aggcttggcc acctcatggt ctaggt                         96
```

<210> 102
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
     Oligonucleotide Primer

<400> 102
```
gacaggggca gtaatgccat ttgc                                      24
```

<210> 103
<211> 177
<212> DNA
<213> human

<400> 103
```
aggtaaggtg tggggGcctg gggctcacct cacagctggg cagctcaccc acagcactgg 60
tacacaccat ccccggcaga atagggctgc catcaccccc aggagctgca tgcagccggc 120
tgcaggccct aggccccagg agggtcacgg gcactgtctg gagggagctg atgcctg    177
```

<210> 104
<211> 63
<212> DNA

<213> human

<400> 104
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att   63

<210> 105
<211> 1443
<212> DNA
<213> human

<400> 105
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agtgtgagga ggcaaggagc ccacatctgc agcggctccc tggtggcaga cacctgggtc 180
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gccctgcagt tgcccagggc ctataaccac tacagccagg gctcagacct ggccctgctg 360
cagctcgccc accccacgac ccacacaccc ctctgcctgc cccagcccgc ccatcgcttc 420
ccctttggag cctcctgctg ggccactggc tgggatcagg acaccagtga tgctcctggg 480
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gcc   1443

<210> 106
<211> 186
<212> DNA
<213> human

<400> 106
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gctatcaacg tgagcctgat gtggctcagt ttccggaagg tccaagaacc ccagggcaag 180
gctaag   186

<210> 107
<211> 599
<212> DNA
<213> human

<400> 107

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gaccaccacc tgcctgatgg ggagcgtggc tgggttctgg acgggcccg cccaggagca 120
ggcatcagct ccctccagac agtgcccgtg accctcctgg ggcctagggc ctgcagccgg 180
ctgcatgcag ctcctggggg tgatggcagc cctattctgc cggggatggt gtgtaccagt 240
gctgtgggtg agctgcccag ctgtgagggc ctgtctgggg caccactggt gcatgaggtg 300
aggggcacat ggttcctggc cgggctgcac agcttcggag atgcttgcca aggccccgcc 360
aggccggcgg tcttcaccgc gctccctgcc tatgaggact gggtcagcag tttggactgg 420
caggtctact tcgccgagga accagagccc gaggctgagc ctggaagctg cctggccaac 480
ataagccaac caaccagctg ctgacagggg acctggccat tctcaggaca agagaatgca 540
ggcaggcaaa tggcattact gcccctgtcc tccccaccct gtcatgtgtg attccaggc 599
```

<210> 108
<211> 998
<212> DNA
<213> human

<400> 108

```
ggacaccagt gatgctcctg ggaccctacg caatctgcgc ctgcgtctca tcagtcgccc 60
cacatgtaac tgtatctaca accagctgca ccagcgacac ctgtccaacc cggcccggcc 120
tgggatgcta tgtggggggcc cccagcctgg ggtgcagggc ccctgtcagg tctgataggg 180
agaagagaag gagcagaagg ggagggggcct aaccctgggc tggggttgg actcacagga 240
ctgggggaaa gagctgcaat cagagggtgt ctgccatagc tgggctcagg catctgtcct 300
tggctttgtt gcctggctcc agggagattc cgggggccct gtgctgtgcc tcgagcctga 360
cggacactgg gttcaggctg gcatcatcag ctttgcatca agctgtgccc aggaggacgc 420
tcctgtgctg ctgaccaaca cagctgctca cagttcctgg ctgcaggctc gagttcaggg 480
ggcagctttc ctggcccaga gcccagagac cccggagatg agtgatgagg acagctgtgt 540
agcctgtgga tccttgagga cagcaggtcc ccaggcagga gcaccctccc catggccctg 600
ggaggccagg ctgatgcacc agggacagct ggcctgtggc ggagccctgg tgtcagagga 660
ggcggtgcta actgctgccc actgcttcat tgggcgccag gccccagagg aatggagcgt 720
agggctgggg accagaccgg aggagtgggg cctgaagcag ctcatcctgc atggagccta 780
cacccaccct gaggggggct acgacatggc cctcctgctg ctggcccagc ctgtgacact 840
gggagccagc ctgcggcccc tctgcctgcc ctatgctgac caccacctgc ctgatgggga 900
gcgtggctgg gttctgggac gggcccgccc aggagcaggc atcagctccc tccagacagt 960
gcccgtgacc ctcctggggc ctagggcctg cagccggc 998
```

<210> 109
<211> 599
<212> DNA
<213> human

<400> 109

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gaccaccacc tgcctgatgg ggagcgtggc tgggttctgg acgggcccg cccaggagca 120
ggcatcagct ccctccagac agtgcccgtg accctcctgg ggcctagggc ctgcagccgg 180
ctgcatgcag ctcctggggg tgatggcagc cctattctgc cggggatggt gtgtaccagt 240
gctgtgggtg agctgcccag ctgtgagggc ctgtctgggg caccactggt gcatgaggtg 300
aggggcacat ggttcctggc cgggctgcac agcttcggag atgcttgcca aggccccgcc 360
aggccggcgg tcttcaccgc gctccctgcc tatgaggact gggtcagcag tttggactgg 420
caggtctact tcgccgagga accagagccc gaggctgagc ctggaagctg cctggccaac 480
ataagccaac caaccagctg ctgacagggg acctggccat tctcaggaca agagaatgca 540
ggcaggcaaa tggcattact gcccctgtcc tccccaccct gtcatgtgtg attccaggc 599
```

<210> 110

<211> 666
<212> DNA
<213> human

<400> 110
```
ccctccccat ggccctggga ggccaggctg atgcaccagg gacagctggc ctgtggcgga 60
gccctggtgt cagaggaggc ggtgctaact gctgcccact gcttcattgg gcgccaggcc 120
ccagaggaat ggagcgtagg gctggggacc agaccggagg agtgggggcct gaagcagctc 180
atcctgcatg gagcctacac ccaccctgag gggggctacg acatggcccct cctgctgctg 240
gcccagcctg tgacactggg agccagcctg cggcccctct gcctgcccta tgctgaccac 300
cacctgcctg atggggagcg tggctgggtt ctgggacggg cccgcccagg agcaggcatc 360
agctccctcc agacagtgcc cgtgaccctc ctggggccta gggcctgcag ccggctgcat 420
gcagctcctg ggggtgatgg cagccctatt ctgccgggga tggtgtgtac cagtgctgtg 480
ggtgagctgc ccagctgtga gggcctgtct ggggcaccac tggtgcatga ggtgaggggc 540
acatggttcc tggccgggct gcacagcttc ggagatgctt gccaaggccc cgccaggccg 600
gcggtcttca ccgcgctccc tgcctatgag gactgggtca gcagtttgga ctggcaggtc 660
tacttc                                                              666
```

<210> 111
<211> 242
<212> PRT
<213> human

<400> 111
```
Pro Gln Ala Gly Ala Pro Ser Pro Trp Pro Trp Glu Ala Arg Leu Met
1               5                   10                  15

His Gln Gly Gln Leu Ala Cys Gly Gly Ala Leu Val Ser Glu Glu Ala
                20                  25                  30

Val Leu Thr Ala Ala His Cys Phe Ile Gly Arg Gln Ala Pro Glu Glu
            35                  40                  45

Trp Ser Val Gly Leu Gly Thr Arg Pro Glu Glu Trp Gly Leu Lys Gln
        50                  55                  60

Leu Ile Leu His Gly Ala Tyr Thr His Pro Glu Gly Gly Tyr Asp Met
65                  70                  75                  80

Ala Leu Leu Leu Leu Ala Gln Pro Val Thr Leu Gly Ala Ser Leu Arg
                85                  90                  95

Pro Leu Cys Leu Pro Tyr Pro Asp His His Leu Pro Asp Gly Glu Arg
                100                 105                 110

Gly Trp Val Leu Gly Arg Ala Arg Pro Gly Ala Gly Ile Ser Ser Leu
            115                 120                 125

Gln Thr Val Pro Val Thr Leu Leu Gly Pro Arg Ala Cys Ser Arg Leu
        130                 135                 140

His Ala Ala Pro Gly Gly Asp Gly Ser Pro Ile Leu Pro Gly Met Val
145                 150                 155                 160

Cys Thr Ser Ala Val Gly Glu Leu Pro Ser Cys Glu Gly Leu Ser Gly
                165                 170                 175
```

86

```
Ala Pro Leu Val His Glu Val Arg Gly Thr Trp Phe Leu Ala Gly Leu
            180                 185                 190

His Ser Phe Gly Asp Ala Cys Gln Gly Pro Ala Arg Pro Ala Val Phe
            195                 200                 205

Thr Ala Leu Pro Ala Tyr Glu Asp Trp Val Ser Ser Leu Asp Trp Gln
    210                 215                 220

Val Tyr Phe Ala Glu Glu Pro Glu Pro Glu Ala Glu Pro Gly Ser Cys
225                 230                 235                 240

Leu Ala
```

```
<210> 112
<211> 242
<212> PRT
<213> human

<400> 112
Pro Gln Ala Gly Ala Pro Ser Pro Trp Pro Trp Glu Ala Arg Leu Met
  1           5                 10                  15

His Gln Gly Gln Leu Ala Cys Gly Gly Ala Leu Val Ser Glu Glu Ala
            20                  25                  30

Val Leu Thr Ala Ala His Cys Phe Ile Gly Arg Gln Ala Pro Glu Glu
            35                  40                  45

Trp Ser Val Gly Leu Gly Thr Arg Pro Glu Glu Trp Gly Leu Lys Gln
    50                  55                  60

Leu Ile Leu His Gly Ala Tyr Thr His Pro Glu Gly Gly Tyr Asp Met
65                  70                  75                  80

Ala Leu Leu Leu Leu Ala Gln Pro Val Thr Leu Gly Ala Ser Leu Arg
                85                  90                  95

Pro Leu Cys Leu Pro Tyr Ala Asp His His Leu Pro Asp Gly Glu Arg
            100                 105                 110

Gly Trp Val Leu Gly Arg Ala Arg Pro Gly Ala Gly Ile Ser Ser Leu
            115                 120                 125

Gln Thr Val Pro Val Thr Leu Leu Gly Pro Arg Ala Cys Ser Arg Leu
    130                 135                 140

His Ala Ala Pro Gly Gly Asp Gly Ser Pro Ile Leu Pro Gly Met Val
145                 150                 155                 160

Cys Thr Ser Ala Val Gly Glu Leu Pro Ser Cys Glu Gly Leu Ser Gly
                165                 170                 175

Ala Pro Leu Val His Glu Val Arg Gly Thr Trp Phe Leu Ala Gly Leu
```

```
              180                  185                      190
His Ser Phe Gly Asp Ala Cys Gln Gly Pro Ala Arg Pro Ala Val Phe
        195                  200                      205
```

```
Thr Ala Leu Pro Ala Tyr Glu Asp Trp Val Ser Ser Leu Asp Trp Gln
    210                  215                      220
```

```
Val Tyr Phe Ala Glu Glu Pro Glu Pro Glu Ala Glu Pro Gly Ser Cys
225                  230                      235              240
```

```
Leu Ala
```

<210> 113
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
      Oligonucleotide Primer

<400> 113
ctgctgacca acacagctgc tcac   24

<210> 114
<211> 844
<212> DNA
<213> human

<400> 114
```
ctgctggccc agcctgtgac actgggagcc agcctgcggc ccctctgcct gccctatcct 60
gaccaccacc tgcctgatgg ggagcgtggc tgggttctgg acgggcccg cccaggagca 120
ggcatcagct ccctccagac agtgcccgtg accctcctgg ggcctagggc ctgcagccgg 180
ctgcatgcag ctcctggggg tgatggcagc cctattctgc cggggatggt gtgtaccagt 240
gctgtgggtg agctgcccag ctgtgagggc ctgtctgggg caccactggt gcatgaggtg 300
aggggcacat ggttcctggc cgggctgcac agcttcggag atgcttgcca aggccccgcc 360
aggccggcgg tcttcaccgc gctccctgcc tatgaggact gggtcagcag tttggactgg 420
caggtctact tcgccgagga accagagccc gaggctgagc ctggaagctg cctggccaac 480
ataagccaac caaccagctg ctgacagggg acctggccat tctcaggaca agagaatgca 540
ggcaggcaaa tggcattact gcccctgtcc tccccaccct gtcatgtgtg attccaggca 600
ccagggcagg cccagaagcc cagcagctgt gggaaggaac ctgcctgggg ccacaggtgc 660
ccactccccca ccctgcagga caggggtgtc tgtggacact cccacaccca actctgctac 720
caagcaggcg tctcagcttt cctcctcctt tactctttca gatacaatca cgccagccac 780
gttgtttga aaatttcttt ttttgggggg cagcagtttt cctttttta aacttaaata 840
aatt                                                             844
```

<210> 115
<211> 587
<212> DNA
<213> human

<400> 115

```
   gcgtgcctgt ggacagcgtg gccccggccc ccccaagcct caggagggca acacagtccc 60
   tggcgagtgg ccctggcagg ccagtgtgag gaggcaagga gcccacatct gcagcggctc 120
   cctggtggca gacacctggg tcctcactgc tgcccactgc tttgaaaagg cagcagcaac 180
   agaactgaat tcctggtcag tggtcctggg ttctctgcag cgtgagggac tcagccctgg 240
   ggccgaagag gtgggggtgg ctgccctgca gttgcccagg gcctataacc actacagcca 300
   gggctcagac ctggccctgc tgcagctcgc ccaccccacg acccacacac ccctctgcct 360
   gccccagccc gcccatcgct tcccctttgg agcctcctgc tgggccactg gctgggatca 420
   ggacaccagt gatgctcctg ggaccctacg caatctgcgc ctgcgtctca tcagtcgccc 480
   cacatgtaac tgtatctaca accagctgca ccagcgacac ctgtccaacc cggcccggcc 540
   tgggatgcta tgtgggggcc cccagcctgg ggtgcagggc ccctgtc          587


   <210> 116
   <211> 844
   <212> DNA
   <213> human

   <400> 116
   ctgctggccc agcctgtgac actgggagcc agcctgcggc ccctctgcct gccctatgct 60
   gaccaccacc tgcctgatgg ggagcgtggc tgggttctgg gacgggcccg cccaggagca 120
   ggcatcagct ccctccagac agtgcccgtg accctcctgg ggcctagggc ctgcagccgg 180
   ctgcatgcag ctcctggggg tgatggcagc cctattctgc cggggatggt gtgtaccagt 240
   gctgtgggtg agcttgccca gctgtgagggc ctgtctgggg caccactggt gcatgaggtg 300
   aggggcacat ggttcctggc cgggctccct gcc tatgaggact gggtcagcag tttggactgg 420
   caggtctact tcgccgagga accagagccc gaggctgagc ctggaagctg cctggccaac 480
   ataagccaac caaccagctg ctgacagggg acctggccat tctcaggaca agagaatgca 540
   ggcaggcaaa tggcattact gcccctgtcc tccccaccct gtcatgtgtg attccaggca 600
   ccagggcagg cccagaagcc cagcagctgt gggaaggaac ctgcctgggg ccacaggtgc 660
   ccactcccca ccctgcagga caggggtgtc tgtggacact cccacaccca actctgctac 720
   caagcaggcg tctcagcttt cctcctcctt tacccttttca gatacaatca cgccagccac 780
   gttgtttttga aaatttcttt ttttgggggg cagcagtttt cctttttttta aacttaaata 840
   aatt                                                          844


   <210> 117
   <211> 1017
   <212> DNA
   <213> human

   <400> 117
   agcgacacct gtccaacccg gcccggcctg ggatgctatg tggggggcccc cagcctgggg 60
   tgcagggccc ctgtcaggtc tgatagggag aagagaagga gcagaagggg aggggcctaa 120
   ccctgggctg ggggttggac tcacaggact gggggaaaga gctgcaatca gagggtgtct 180
   gccatagctg ggctcaggca tctgtccttg gctttgttgc ctggctccag ggagattccg 240
   ggggccctgt gctgtgcctc gagcctgacg gacactgggt tcaggctggc atcatcagct 300
   ttgcatcaag ctgtgcccag gaggacgctc ctgtgctgct gaccaacaca gctgctcaca 360
   gttcctggct gcaggctcga gttcaggggg cagctttcct ggcccagagc ccagagaccc 420
   cggagatgag tgatgaggac agctgtgtag cctgtggatc cttgaggaca gcaggtcccc 480
   aggcaggagc accctcccca tggccctggg aggccaggct gatgcaccag ggacagctgg 540
   cctgtggcgg agccctggtg tcagaggagg cggtgctaac tgctgcccac tgcttcattg 600
   ggcgccaggc cccagaggaa tggagcgtag ggctggggac cagaccggag gagtgggggcc 660
   tgaagcagct catcctgcat ggagcctaca cccaccctga gggggggctac gacatggccc 720
   tcctgctgct ggcccagcct gtgacactgg agccagcct gcggcccctc tgcctgccct 780
   atgctgacca ccacctgcct gatggggagc gtggctgggt tctgggacgg gcccgcccag 840
   gagcaggcat cagctccctc cagacagtgc ccgtgaccct cctgggggcct aggggcctgca 900
   gccggctgca tgcagctcct gggggtgatg gcagccctat tctgccgggg atggtgtgta 960
```

ccagtgctgt gggtgagctg cccagctgtg agggcctgtc tggggcacca ctggtgc   1017

<210> 118
<211> 203
<212> PRT
<213> human

<400> 118
Pro Gly Glu Trp Pro Trp Gln Ala Ser Val Arg Arg Gln Gly Ala His
1   5   10   15

Ile Cys Ser Gly Ser Leu Val Ala Asp Thr Trp Val Leu Thr Ala Ala
            20   25   30

His Cys Phe Glu Lys Ala Ala Ala Thr Glu Leu Asn Ser Trp Ser Val
        35   40   45

Val Leu Gly Ser Leu Gln Arg Glu Gly Leu Ser Pro Gly Ala Glu Glu
    50   55   60

Val Gly Val Ala Ala Leu Gln Leu Pro Arg Ala Tyr Asn His Tyr Ser
65   70   75   80

Gln Gly Ser Asp Leu Ala Leu Leu Gln Leu Ala His Pro Thr Thr His
            85   90   95

Thr Pro Leu Cys Leu Pro Gln Pro Ala His Arg Phe Pro Phe Gly Ala
            100   105   110

Ser Cys Trp Ala Thr Gly Trp Asp Gln Asp Thr Ser Asp Ala Pro Gly
        115   120   125

Thr Leu Arg Asn Leu Arg Leu Arg Leu Ile Ser Arg Pro Thr Cys Asn
    130   135   140

Cys Ile Tyr Asn Gln Leu His Gln Arg His Leu Ser Asn Pro Ala Arg
145   150   155   160

Pro Gly Met Leu Cys Gly Gly Pro Gln Pro Gly Val Gln Gly Pro Cys
            165   170   175

Gln Gly Asp Ser Gly Gly Pro Val Leu Cys Leu Glu Pro Asp Gly His
            180   185   190

Trp Val Gln Ala Gly Ile Ile Ser Phe Ala Ser
        195   200

<210> 119
<211> 90
<212> PRT
<213> human

<400> 119
Ser Pro Ile Leu Pro Gly Met Val Cys Thr Ser Ala Val Gly Glu Leu
1   5   10   15

90

```
Pro Ser Cys Glu Gly Leu Ser Gly Ala Pro Leu Val His Glu Val Arg
            20                  25                  30
```

```
Gly Thr Trp Phe Leu Ala Gly Leu His Ser Phe Gly Asp Ala Cys Gln
            35                  40                  45
```

```
Gly Pro Ala Arg Pro Ala Val Phe Thr Ala Leu Pro Ala Tyr Glu Asp
        50              55                  60
```

```
Trp Val Ser Ser Leu Asp Trp Gln Val Tyr Phe Ala Glu Glu Pro Glu
65                  70                  75                      80
```

```
Pro Glu Ala Glu Pro Gly Ser Cys Leu Ala
                    85              90
```

<210> 120
<211> 90
<212> PRT
<213> human

<400> 120
```
Ser Pro Ile Leu Pro Gly Met Val Cys Thr Ser Ala Val Gly Glu Leu
    1               5                  10                  15
```

```
Pro Ser Cys Glu Gly Leu Ser Gly Ala Pro Leu Val His Glu Val Arg
            20                  25                  30
```

```
Gly Thr Trp Phe Leu Ala Gly Leu His Ser Phe Gly Asp Ala Cys Gln
            35                  40                  45
```

```
Gly Pro Ala Arg Pro Ala Val Phe Thr Ala Leu Pro Ala Tyr Glu Asp
        50              55                  60
```

```
Trp Val Ser Ser Leu Asp Trp Gln Val Tyr Phe Ala Glu Glu Pro Glu
65                  70                  75                      80
```

```
Pro Glu Ala Glu Pro Gly Ser Cys Leu Ala
                85              90
```

<210> 121
<211> 177
<212> DNA
<213> human

<400> 121
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aggtaaggtg tggggggcctg gggctcacct cacagctggg cagctcaccc acagcactgg 60
tacacaccat ccccggcaga atagggctgc catcaccccc aggagctgca tgcagccggc 120
tgcaggccct aggccccagg agggtcacgg gcactgtctg gagggagctg atgcctg    177
```

<210> 122
<211> 571
<212> PRT
<213> human

<400> 122

```
Met Leu Leu Ser Ser Leu Val Ser Leu Ala Gly Ser Val Tyr Leu Ala
 1               5                  10                  15

Trp Ile Leu Phe Phe Val Leu Tyr Asp Phe Cys Ile Val Cys Ile Thr
            20              25                  30

Thr Tyr Ala Ile Asn Val Ser Leu Met Trp Leu Ser Phe Arg Lys Val
        35              40                  45

Gln Glu Pro Gln Gly Lys Ala Lys Arg His Gly Asn Thr Val Pro Gly
    50              55                  60

Glu Trp Pro Trp Gln Ala Ser Val Arg Arg Gln Gly Ala His Ile Cys
65              70                  75                  80

Ser Gly Ser Leu Val Ala Asp Thr Trp Val Leu Thr Ala Ala His Cys
            85                  90                  95

Phe Glu Lys Ala Ala Ala Thr Glu Leu Asn Ser Trp Ser Val Val Leu
        100             105                 110

Gly Ser Leu Gln Arg Glu Gly Leu Ser Pro Gly Ala Glu Glu Val Gly
        115             120                 125

Val Ala Ala Leu Gln Leu Pro Arg Ala Tyr Asn His Tyr Ser Gln Gly
    130             135                 140

Ser Asp Leu Ala Leu Leu Gln Leu Ala His Pro Thr Thr His Thr Pro
145             150                 155                 160

Leu Cys Leu Pro Gln Pro Ala His Arg Phe Pro Phe Gly Ala Ser Cys
            165             170                 175

Trp Ala Thr Gly Trp Asp Gln Asp Thr Ser Asp Ala Pro Gly Thr Leu
            180             185                 190

Arg Asn Leu Arg Leu Arg Leu Ile Ser Arg Pro Thr Cys Asn Cys Ile
        195             200                 205

Tyr Asn Gln Leu His Gln Arg His Leu Ser Asn Pro Ala Arg Pro Gly
    210             215                 220

Met Leu Cys Gly Gly Pro Gln Pro Gly Val Gln Gly Pro Cys Gln Gly
225             230                 235                 240

Asp Ser Gly Gly Pro Val Leu Cys Leu Glu Pro Asp Gly His Trp Val
            245             250                 255

Gln Ala Gly Ile Ile Ser Phe Ala Ser Ser Cys Ala Gln Glu Asp Ala
            260             265                 270

Pro Val Leu Leu Thr Asn Thr Ala Ala His Ser Ser Trp Leu Gln Ala
        275             280                 285

Arg Val Gln Gly Ala Ala Phe Leu Ala Gln Ser Pro Glu Thr Pro Glu
```

92

```
     290                       295                        300

Met Ser Asp Glu Asp Ser Cys Val Ala Cys Gly Ser Leu Arg Thr Ala
305                 310                 315                 320

Gly Pro Gln Ala Gly Ala Pro Ser Pro Trp Pro Trp Glu Ala Arg Leu
                325                 330                 335

Met His Gln Gly Gln Leu Ala Cys Gly Gly Ala Leu Val Ser Glu Glu
                340                 345                 350

Ala Val Leu Thr Ala Ala His Cys Phe Ile Gly Arg Gln Ala Pro Glu
                355                 360                 365

Glu Trp Ser Val Gly Leu Gly Thr Arg Pro Glu Glu Trp Gly Leu Lys
370                 375                 380

Gln Leu Ile Leu His Gly Ala Tyr Thr His Pro Glu Gly Gly Tyr Asp
385                 390                 395                 400

Met Ala Leu Leu Leu Leu Ala Gln Pro Val Thr Leu Gly Ala Ser Leu
                405                 410                 415

Arg Pro Leu Cys Leu Pro Tyr Pro Asp His His Leu Pro Asp Gly Glu
                420                 425                 430

Arg Gly Trp Val Leu Gly Arg Ala Arg Pro Gly Ala Gly Ile Ser Ser
                435                 440                 445

Leu Gln Thr Val Pro Val Thr Leu Leu Gly Pro Arg Ala Cys Ser Arg
                450                 455                 460

Leu His Ala Ala Pro Gly Gly Asp Gly Ser Pro Ile Leu Pro Gly Met
465                 470                 475                 480

Val Cys Thr Ser Ala Val Gly Glu Leu Pro Ser Cys Glu Gly Leu Ser
                485                 490                 495

Gly Ala Pro Leu Val His Glu Val Arg Gly Thr Trp Phe Leu Ala Gly
                500                 505                 510

Leu His Ser Phe Gly Asp Ala Cys Gln Gly Pro Ala Arg Pro Ala Val
                515                 520                 525

Phe Thr Ala Leu Pro Ala Tyr Glu Asp Trp Val Ser Ser Leu Asp Trp
530                 535                 540

Gln Val Tyr Phe Ala Glu Glu Pro Glu Pro Glu Ala Glu Pro Gly Ser
545                 550                 555                 560

Cys Leu Ala Asn Ile Ser Gln Pro Thr Ser Cys
                565                 570
```

<210> human

<400> 123

```
Met Ser Asp Glu Asp Ser Cys Val Ala Cys Gly Ser Leu Arg Thr Ala
1               5                   10                  15

Gly Pro Gln Ala Gly Ala Pro Ser Pro Trp Pro Trp Glu Ala Arg Leu
                20                  25                  30

Met His Gln Gly Gln Leu Ala Cys Gly Gly Ala Leu Val Ser Glu Glu
        35                  40                  45

Ala Val Leu Thr Ala Ala His Cys Phe Ile Gly Arg Gln Ala Pro Glu
        50                  55                  60

Glu Trp Ser Val Gly Leu Gly Thr Arg Pro Glu Glu Trp Gly Leu Lys
65                  70                  75                  80

Gln Leu Ile Leu His Gly Ala Tyr Thr His Pro Glu Gly Gly Tyr Asp
                85                  90                  95

Met Ala Leu Leu Leu Leu Ala Gln Pro Val Thr Leu Gly Ala Ser Leu
            100                 105                 110

Arg Pro Leu Cys Leu Pro Tyr Ala Asp His His Leu Pro Asp Gly Glu
            115                 120                 125

Arg Gly Trp Val Leu Gly Arg Ala Arg Pro Gly Ala Gly Ile Ser Ser
    130                 135                 140

Leu Gln Thr Val Pro Val Thr Leu Leu Gly Pro Arg Ala Cys Ser Arg
145                 150                 155                 160

Leu His Ala Ala Pro Gly Gly Asp Gly Ser Pro Ile Leu Pro Gly Met
                165                 170                 175

Val Cys Thr Ser Ala Val Gly Glu Leu Pro Ser Cys Glu Gly Leu Ser
            180                 185                 190

Gly Ala Pro Leu Val His Glu Val Arg Gly Thr Trp Phe Leu Ala Gly
            195                 200                 205

Leu His Ser Phe Gly Asp Ala Cys Gln Gly Pro Ala Arg Pro Ala Val
    210                 215                 220

Phe Thr Ala Leu Pro Ala Tyr Glu Asp Trp Val Ser Ser Leu Asp Trp
225                 230                 235                 240

Gln Val Tyr Phe Ala Glu Glu Pro Glu Pro Glu Ala Glu Pro Gly Ser
                245                 250                 255

Cys Leu Ala Asn Ile Ser Gln Pro Thr Ser Cys
                260                 265
```

<210> 124
<211> 314

94

<212> PRT
<213> human

<400> 124

Met Gly Ala Arg Gly Ala Leu Leu Leu Ala Leu Leu Leu Ala Arg Ala
1   5   10   15

Gly Leu Arg Lys Pro Glu Ser Gln Glu Ala Ala Pro Leu Ser Gly Pro
                20   25   30

Cys Gly Arg Arg Val Ile Thr Ser Arg Ile Val Gly Gly Glu Asp Ala
            35   40   45

Glu Leu Gly Arg Trp Pro Trp Gln Gly Ser Leu Arg Leu Trp Asp Ser
    50   55   60

His Val Cys Gly Val Ser Leu Leu Ser His Arg Trp Ala Leu Thr Ala
65   70   75   80

Ala His Cys Phe Glu Thr Tyr Ser Asp Leu Ser Asp Pro Ser Gly Trp
                85   90   95

Met Val Gln Phe Gly Gln Leu Thr Ser Met Pro Ser Phe Trp Ser Leu
            100   105   110

Gln Ala Tyr Tyr Thr Arg Tyr Phe Val Ser Asn Ile Tyr Leu Ser Pro
            115   120   125

Arg Tyr Leu Gly Asn Ser Pro Tyr Asp Ile Ala Leu Val Lys Leu Ser
130   135   140

Ala Pro Val Thr Tyr Thr Lys His Ile Gln Pro Ile Cys Leu Gln Ala
145   150   155   160

Ser Thr Phe Glu Phe Glu Asn Arg Thr Asp Cys Trp Val Thr Gly Trp
                165   170   175

Gly Tyr Ile Lys Glu Asp Glu Ala Leu Pro Ser Pro His Thr Leu Gln
            180   185   190

Glu Val Gln Val Ala Ile Ile Asn Asn Ser Met Cys Asn His Leu Phe
            195   200   205

Leu Lys Tyr Ser Phe Arg Lys Asp Ile Phe Gly Asp Met Val Cys Ala
    210   215   220

Gly Asn Ala Gln Gly Gly Lys Asp Ala Cys Phe Gly Asp Ser Gly Gly
225   230   235   240

Pro Leu Ala Cys Asn Lys Asn Gly Leu Trp Tyr Gln Ile Gly Val Val
            245   250   255

Ser Trp Gly Val Gly Cys Gly Arg Pro Asn Arg Pro Gly Val Tyr Thr
            260   265   270

Asn Ile Ser His His Phe Glu Trp Ile Gln Lys Leu Met Ala Gln Ser
    275   280   285

95

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Gly Met Ser Gln Pro Asp Pro Ser Trp Pro Leu Leu Phe Phe Pro Leu
    290             295         300
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Leu Trp Ala Leu Pro Leu Leu Gly Pro Val
305             310
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<212> PRT
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<400> 125
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Ile Leu Leu Tyr Leu Gly Leu Leu Arg Ser Gly Thr Gly Ala Glu Gly
            20              25              30
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Ala Glu Ala Pro Cys Gly Val Ala Pro Gln Ala Arg Ile Thr Gly Gly
        35              40              45
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Ser Ser Ala Val Ala Gly Gln Trp Pro Trp Gln Val Ser Ile Thr Tyr
    50              55              60
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Glu Gly Val His Val Cys Gly Gly Ser Leu Val Ser Glu Gln Trp Val
65              70              75              80
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Leu Ser Ala Ala His Cys Phe Pro Ser Glu His His Lys Glu Ala Tyr
                85              90              95
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Glu Val Lys Leu Gly Ala His Gln Leu Asp Ser Tyr Ser Glu Asp Ala
            100             105             110
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Lys Val Ser Thr Leu Lys Asp Ile Ile Pro His Pro Ser Tyr Leu Gln
            115             120             125
```

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Glu Gly Ser Gln Gly Asp Ile Ala Leu Leu Gln Leu Ser Arg Pro Ile
    130             135             140
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Thr Phe Ser Arg Tyr Ile Arg Pro Ile Cys Leu Pro Ala Ala Asn Ala
145             150             155             160
```

```
Ser Phe Pro Asn Gly Leu His Cys Thr Val Thr Gly Trp Gly His Val
                165             170             175
```

```
Ala Pro Ser Val Ser Leu Leu Thr Pro Lys Pro Leu Gln Gln Leu Glu
            180             185             190
```

```
Val Pro Leu Ile Ser Arg Glu Thr Cys Asn Cys Leu Tyr Asn Ile Asp
    195             200             205
```

```
Ala Lys Pro Glu Glu Pro His Phe Val Gln Glu Asp Met Val Cys Ala
    210             215             220
```

```
Gly Tyr Val Glu Gly Gly Lys Asp Ala Cys Gln Gly Asp Ser Gly Gly
```

```
Pro Leu Ser Cys Pro Val Glu Gly Leu Trp Tyr Leu Thr Gly Ile Val
            245                 250                 255

Ser Trp Gly Asp Ala Cys Gly Ala Arg Asn Arg Pro Gly Val Tyr Thr
            260                 265                 270

Leu Ala Ser Ser Tyr Ala Ser Trp Ile Gln Ser Lys Val Thr Glu Leu
            275                 280                 285

Gln Pro Arg Val Val Pro Gln Thr Gln Glu Ser Gln Pro Asp Ser Asn
    290                 295                 300

Leu Cys Gly Ser His Leu Ala Phe Ser Ser Ala Pro Ala Gln Gly Leu
305                 310                 315                 320

Leu Arg Pro Ile Leu Phe Leu Pro Leu Gly Leu Ala Leu Gly Leu Leu
            325                 330                 335

Ser Pro Trp Leu Ser Glu His
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<211> 69
<212> PRT
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<220>
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      Protein Signature Sequence

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Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
        20   25   30

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
    35   40   45

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Xaa Xaa Xaa Xaa Xaa
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gccccgccag gtcttccaga agattccctt cttaagcttc tgccgctgct gtgggatgga 180
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<211> 245
<212> DNA
<213> human

<400> 128
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gccccgccag gtcttccaga agattccctt cttaagcttc tgccgctgct gtgggatgga 180
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gaggc 245

<210> 129
<211> 91
<212> DNA
<213> human

<400> 129
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tggcgcctct gaattaatgt ccactctgcc t 91

<210> 130
<211> 413
<212> DNA

<213> human

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ggtggtggcg cccagctggc cggccacggg tgcagtgagc tgcaggctat aggccgtgtc 180
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ctgcacggcc aggcggctgt tgcggtcccc cgtgatgcta tgcaccttct ccagacccag 300
ccagaactcg ccgtgggggat ccccaaaccc cgccttgtag cttcccagg gccggttgaa 360
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<210> 131
<211> 401
<212> DNA
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<400> 131
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gatggagcgg aagtactggc cgttgaggtt ggaatggctg caggtgccaa accaccagcc 180
tccagagagg ctcttggcgc agttcttgtc cctgcggagg tcgtgatcct ggtcccaagt 240
ggagaagggt acggagaggc cgctgggtgg gacggtggtg gcgcccagct ggccggccac 300
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cagcaactcg gcgttgccat cccagtcccg cagctgcacg g 401

<210> 132
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<212> DNA
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<400> 132
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tggcgcctct gaattaatgt ccactctgcc t 91